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(54) Title: INSECTICIDAL TOXINS FROM PHOTORHABDUS (57) Abstract Novel nucleic acid sequences isolated from <i>Photobhabdus luminescens</i> , whose expression results in novel insecticidal toxins, are disclosed herein. The invention also discloses compositions and formulations containing the insecticidal toxins that are capable of controlling insect pests. The invention is further drawn to methods of making the toxins and to methods of using the nucleotide sequences, for example in microorganisms to control insect pests or in transgenic plants to confer insect resistance.		

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INSECTICIDAL TOXINS FROM PHOTORHABDUS

The invention relates to novel toxins from *Photorhabdus luminescens*, nucleic acid sequences whose expression results in said toxins, and methods of making and methods of using the toxins and corresponding nucleic acid sequences to control insects.

Insect pests are a major cause of crop losses. Solely in the US, about \$7.7 billion are lost every year due to infestation by various genera of insects. In addition to losses in field crops, insect pests are also a burden to vegetable and fruit growers, to producers of ornamental flowers, and they are a nuisance to gardeners and home owners.

Insect pests are mainly controlled by intensive applications of chemical insecticides, which are active through inhibition of insect growth, prevention of insect feeding or reproduction, or death of the insects. Good insect control can thus be reached, but these chemicals can sometimes also affect other, beneficial insects. Another problem resulting from the wide use of chemical pesticides is the appearance of resistant insect varieties. This has been partially alleviated by various resistance management strategies, but there is an increasing need for alternative pest control agents. Biological insect control agents, such as *Bacillus thuringiensis* strains expressing insecticidal toxins like d-endotoxins, have also been applied with satisfactory results, offering an alternative or a complement to chemical insecticides. Recently, the genes coding for some of these d-endotoxins have been isolated and their expression in heterologous hosts have been shown to provide another tool for the control of economically important insect pests. In particular, the expression of insecticidal toxins in transgenic plants, such as *Bacillus thuringiensis* d-endotoxins, has provided efficient protection against selected insect pests, and transgenic plants expressing such toxins have been commercialized, allowing farmers to reduce applications of chemical insect control agents. Yet, even in this case, the development of resistance remains a possibility and only a few specific insect pests are controllable. Consequently, there remains a long-felt but unfulfilled need to discover new and effective insect control agents that provide an economic benefit to farmers and that are environmentally acceptable.

The present invention addresses the need for novel insect control agents. Particularly needed are control agents that are targeted to economically important insect pests and that efficiently control insect strains resistant to existing insect control agents.

Furthermore, agents whose application minimizes the burden on the environment are desirable.

In the search of novel insect control agents, certain classes of nematodes from the genera *Heterorhabdus* and *Steinernema* are of particular interest because of their insecticidal properties. They kill insect larvae and their offspring feed in the dead larvae. Indeed, the insecticidal activity is due to symbiotic bacteria living in the nematodes. These symbiotic bacteria are *Photorhabdus* in the case of *Heterorhabdus* and *Xenorhabdus* in the case of *Steinernema*.

The present invention is drawn to nucleic acid sequences isolated from *Photorhabdus luminescens*, and sequences substantially similar thereto, whose expression results in toxins that are highly toxic to economically important insect pests, particularly insect pests that infest plants. The invention is further drawn to the toxins resulting from the expression of the nucleic acid sequences, and to compositions and formulations containing the toxins, which are capable of inhibiting the ability of insect pests to survive, grow or reproduce, or of limiting insect-related damage or loss in crop plants. The invention is further drawn to a method of making the toxins and to methods of using the nucleic acid sequences, for example in microorganisms to control insects or in transgenic plants to confer insect resistance, and to a method of using the toxins, and compositions and formulations comprising the toxins, for example applying the toxins or compositions or formulations to insect-infested areas, or to prophylactically treat insect-susceptible areas or plants to confer protection or resistance to the insects.

The novel toxins are highly active against insects. For example, a number of economically important insect pests, such as the Lepidopterans *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Manduca sexta* (Tobacco Hornworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm), as well as the Coleopterans *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle) can be controlled by one or more of the toxins. The toxins can be used in multiple insect control strategies, resulting in maximal efficiency with minimal impact on the environment.

According to one aspect, the present invention provides an isolated nucleic acid molecule comprising: (a) a nucleotide sequence substantially similar to a nucleotide

sequence selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 15,171-18,035 of SEQ ID NO:11, and nucleotides 31,393-35,838 of SEQ ID NO:11; (b) a nucleotide sequence comprising nucleotides 23,768-31,336 of SEQ ID NO:11; or (c) a nucleotide sequence isocoding with the nucleotide sequence of (a) or (b); wherein expression of the nucleic acid molecule results in at least one toxin that is active against insects.

In one embodiment of this aspect, the nucleotide sequence is isocoding with a nucleotide sequence substantially similar to nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1. Preferably, the nucleotide sequence is substantially similar to nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1. More preferably, the nucleotide sequence encodes an amino acid sequence selected from the group consisting of SEQ ID NOs:2-6. Most preferably, the nucleotide sequence comprises nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

In another embodiment of this aspect, the nucleotide sequence is isocoding with a nucleotide sequence substantially similar to nucleotides 15,171-18,035 of SEQ ID NO:11. Preferably, the nucleotide sequence is substantially similar to nucleotides 15,171-18,035 of SEQ ID NO:11. More preferably, the nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NO:12. Most preferably, the nucleotide sequence comprises nucleotides 15,171-18,035 of SEQ ID NO:11.

In still another embodiment of this aspect, the nucleotide sequence is isocoding with a nucleotide sequence substantially similar to nucleotides 31,393-35,838 of SEQ ID NO:11. Preferably, the nucleotide sequence is substantially similar to nucleotides 31,393-35,838 of SEQ ID NO:11. More preferably, the nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NO:14. Most preferably, the nucleotide sequence comprises nucleotides 31,393-35,838 of SEQ ID NO:11.

In yet another embodiment of this aspect, the nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NO:13, and preferably comprises nucleotides 23,768-31,336 of SEQ ID NO:11.

In one embodiment, the nucleotide sequence of the invention comprises the approximately 9.7 kb DNA fragment harbored in *E. coli* strain DH5a, designated as NRRL accession number B-21835.

In another embodiment, the nucleotide sequence of the invention comprises the approximately 38 kb DNA fragment harbored in *E. coli* strain DH5a, designated as NRRL accession number B-30077.

In still another embodiment, the nucleotide sequence of the invention comprises the approximately 22.2 kb DNA fragment harbored in *E. coli* strain DH5a, designated as NRRL accession number B-30078.

According to one embodiment of the invention, the toxins resulting from expression of the nucleic acid molecules of the invention have activity against Lepidopteran insects. Preferably, according to this embodiment, the toxins have activity against *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm).

According to another embodiment of the invention, the toxins resulting from expression of the nucleic acid molecule of the invention have activity against Lepidopteran and Coleopteran insects. Preferably, according to this embodiment, the toxins have insecticidal activity against *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

In another aspect, the present invention provides an isolated nucleic acid molecule comprising a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of a nucleotide sequence selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 15,171-18,035 of SEQ ID NO:11, and nucleotides 31,393-35,838 of SEQ ID NO:11, wherein expression of the nucleic acid molecule results in at least one toxin that is active against insects.

In one embodiment of this aspect, the isolated nucleic acid molecule of the invention comprises a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

In another embodiment of this aspect, the isolated nucleic acid molecule of the invention comprises a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 15,171-18,035 of SEQ ID NO:11.

In still another embodiment of this aspect, the isolated nucleic acid molecule of the invention comprises a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 31,393-35,838 of SEQ ID NO:11.

In a further aspect, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence from *Photobacterium luminescens* selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 66-1898 of SEQ ID NO:11, nucleotides 2416-9909 of SEQ ID NO:11, the complement of nucleotides 2817-3395 of SEQ ID NO:11, nucleotides 9966-14,633 of SEQ ID NO:11, nucleotides 14,699-15,007 of SEQ ID NO:11, nucleotides 15,171-18,035 of SEQ ID NO:11, the complement of nucleotides 17,072-17,398 of SEQ ID NO:11, the complement of nucleotides 18,235-19,167 of SEQ ID NO:11, the complement of nucleotides 19,385-20,116 of SEQ ID NO:11, the complement of nucleotides 20,217-20,963 of SEQ ID NO:11, the complement of nucleotides 22,172-23,086 of SEQ ID NO:11, nucleotides 23,768-31,336 of SEQ ID NO:11, nucleotides 31,393-35,838 of SEQ ID NO:11, the complement of nucleotides 35,383-35,709 of SEQ ID NO:11, the complement of nucleotides 36,032-36,661 of SEQ ID NO:11, and the complement of nucleotides 36,654-37,781 of SEQ ID NO:11.

The present invention also provides a chimeric gene comprising a heterologous promoter sequence operatively linked to the nucleic acid molecule of the invention. Further, the present invention provides a recombinant vector comprising such a chimeric gene. Still further, the present invention provides a host cell comprising such a chimeric gene. A host cell according to this aspect of the invention may be a bacterial cell, a yeast cell, or a plant

cell, preferably a plant cell. Even further, the present invention provides a plant comprising such a plant cell. Preferably, the plant is maize.

In yet another aspect, the present invention provides toxins produced by the expression of DNA molecules of the present invention.

According to one embodiment, the toxins of the invention have activity against Lepidopteran insects, preferably against *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm).

According to another embodiment, the toxins of the invention have activity against Lepidopteran and Coleopteran insects, preferably against *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

In one embodiment, the toxins are produced by the *E. coli* strain designated as NRRL accession number B-21835.

In another embodiment, the toxins are produced by *E. coli* strain designated as NRRL accession number B-30077.

In still another embodiment, the toxins are produced by *E. coli* strain designated as NRRL accession number B-30078.

In one embodiment, a toxin of the invention comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs:2-6.

In another embodiment, a toxin of the invention comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs:12-14.

The present invention also provides a composition comprising an insecticidally effective amount of a toxin according to the invention.

In another aspect, the present invention provides a method of producing a toxin that is active against insects, comprising: (a) obtaining a host cell comprising a chimeric gene, which itself comprises a heterologous promoter sequence operatively linked to the nucleic acid molecule of the invention; and (b) expressing the nucleic acid molecule in the cell, which results in at least one toxin that is active against insects.

In a further aspect, the present invention provides a method of producing an insect-resistant plant, comprising introducing a nucleic acid molecule of the invention into the plant, wherein the nucleic acid molecule is expressible in the plant in an effective amount to control insects. According to one embodiment, the insects are Lepidopteran insects, preferably selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm). According to another embodiment, the insects are Lepidopteran and Coleopteran insects, preferably selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

In still a further aspect, the present invention provides a method of controlling insects comprising delivering to the insects an effective amount of a toxin according to the present invention. According to one embodiment, the insects are Lepidopteran insects, preferably selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm). According to another embodiment, the insects are Lepidopteran and Coleopteran insects, preferably selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle). Preferably, the toxin is delivered to the insects orally.

Yet another aspect of the present invention is the provision of a method for mutagenizing a nucleic acid molecule according to the present invention, wherein the nucleic acid molecule has been cleaved into population of double-stranded random fragments of a desired size, comprising: (a) adding to the population of double-stranded random fragments one or more single- or double-stranded oligonucleotides, wherein the oligonucleotides each comprise an area of identity and an area of heterology to a double-stranded template polynucleotide; (b) denaturing the resultant mixture of double-stranded

random fragments and oligonucleotides into single-stranded fragments; (c) incubating the resultant population of single-stranded fragments with a polymerase under conditions which result in the annealing of the single-stranded fragments at the areas of identity to form pairs of annealed fragments, the areas of identity being sufficient for one member of a pair to prime replication of the other, thereby forming a mutagenized double-stranded polynucleotide; and (d) repeating the second and third steps for at least two further cycles, wherein the resultant mixture in the second step of a further cycle includes the mutagenized double-stranded polynucleotide from the third step of the previous cycle, and wherein the further cycle forms a further mutagenized double-stranded polynucleotide.

Other aspects and advantages of the present invention will become apparent to those skilled in the art from a study of the following description of the invention and non-limiting examples.

DEFINITIONS

"Activity" of the toxins of the invention is meant that the toxins function as orally active insect control agents, have a toxic effect, or are able to disrupt or deter insect feeding, which may or may not cause death of the insect. When a toxin of the invention is delivered to the insect, the result is typically death of the insect, or the insect does not feed upon the source that makes the toxin available to the insect.

"Associated with / operatively linked" refer to two nucleic acid sequences that are related physically or functionally. For example, a promoter or regulatory DNA sequence is said to be "associated with" a DNA sequence that codes for an RNA or a protein if the two sequences are operatively linked, or situated such that the regulator DNA sequence will affect the expression level of the coding or structural DNA sequence.

A "chimeric gene" is a recombinant nucleic acid sequence in which a promoter or regulatory nucleic acid sequence is operatively linked to, or associated with, a nucleic acid sequence that codes for an mRNA or which is expressed as a protein, such that the regulator nucleic acid sequence is able to regulate transcription or expression of the associated nucleic acid sequence. The regulator nucleic acid sequence of the chimeric gene is not normally operatively linked to the associated nucleic acid sequence as found in nature.

A "coding sequence" is a nucleic acid sequence that is transcribed into RNA such as mRNA, rRNA, tRNA, snRNA, sense RNA or antisense RNA. Preferably the RNA is then translated in an organism to produce a protein.

To "control" insects means to inhibit, through a toxic effect, the ability of insect pests to survive, grow, feed, and/or reproduce, or to limit insect-related damage or loss in crop plants. To "control" insects may or may not mean killing the insects, although it preferably means killing the insects.

To "deliver" a toxin means that the toxin comes in contact with an insect, resulting in toxic effect and control of the insect. The toxin can be delivered in many recognized ways, e.g., orally by ingestion by the insect or by contact with the insect via transgenic plant expression, formulated protein composition(s), sprayable protein composition(s), a bait matrix, or any other art-recognized toxin delivery system.

"Expression cassette" as used herein means a nucleic acid sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is heterologous with respect to the host, i.e., the particular nucleic acid sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, such as a plant, the promoter can also be specific to a particular tissue, or organ, or stage of development.

A "gene" is a defined region that is located within a genome and that, besides the aforementioned coding nucleic acid sequence, comprises other, primarily regulatory, nucleic acid sequences responsible for the control of the expression, that is to say the transcription and translation, of the coding portion. A gene may also comprise other 5' and 3'

untranslated sequences and termination sequences. Further elements that may be present are, for example, introns.

"Gene of interest" refers to any gene which, when transferred to a plant, confers upon the plant a desired characteristic such as antibiotic resistance, virus resistance, insect resistance, disease resistance, or resistance to other pests, herbicide tolerance, improved nutritional value, improved performance in an industrial process or altered reproductive capability. The "gene of interest" may also be one that is transferred to plants for the production of commercially valuable enzymes or metabolites in the plant.

A "heterologous" nucleic acid sequence is a nucleic acid sequence not naturally associated with a host cell into which it is introduced, including non-naturally occurring multiple copies of a naturally occurring nucleic acid sequence.

A "homologous" nucleic acid sequence is a nucleic acid sequence naturally associated with a host cell into which it is introduced.

"Homologous recombination" is the reciprocal exchange of nucleic acid fragments between homologous nucleic acid molecules.

"Insecticidal" is defined as a toxic biological activity capable of controlling insects, preferably by killing them.

A nucleic acid sequence is "isocoding with" a reference nucleic acid sequence when the nucleic acid sequence encodes a polypeptide having the same amino acid sequence as the polypeptide encoded by the reference nucleic acid sequence.

An "isolated" nucleic acid molecule or an isolated enzyme is a nucleic acid molecule or enzyme that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated nucleic acid molecule or enzyme may exist in a purified form or may exist in a non-native environment such as, for example, a recombinant host cell.

A "nucleic acid molecule" or "nucleic acid sequence" is a linear segment of single- or double-stranded DNA or RNA that can be isolated from any source. In the context of the present invention, the nucleic acid molecule is preferably a segment of DNA.

"ORF" means open reading frame.

A "plant" is any plant at any stage of development, particularly a seed plant.

A "plant cell" is a structural and physiological unit of a plant, comprising a protoplast and a cell wall. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, plant tissue, a plant organ, or a whole plant.

"Plant cell culture" means cultures of plant units such as, for example, protoplasts, cell culture cells, cells in plant tissues, pollen, pollen tubes, ovules, embryo sacs, zygotes and embryos at various stages of development.

"Plant material" refers to leaves, stems, roots, flowers or flower parts, fruits, pollen, egg cells, zygotes, seeds, cuttings, cell or tissue cultures, or any other part or product of a plant.

A "plant organ" is a distinct and visibly structured and differentiated part of a plant such as a root, stem, leaf, flower bud, or embryo.

"Plant tissue" as used herein means a group of plant cells organized into a structural and functional unit. Any tissue of a plant *in planta* or in culture is included. This term includes, but is not limited to, whole plants, plant organs, plant seeds, tissue culture and any groups of plant cells organized into structural and/or functional units. The use of this term in conjunction with, or in the absence of, any specific type of plant tissue as listed above or otherwise embraced by this definition is not intended to be exclusive of any other type of plant tissue.

A "promoter" is an untranslated DNA sequence upstream of the coding region that contains the binding site for RNA polymerase II and initiates transcription of the DNA. The promoter region may also include other elements that act as regulators of gene expression.

A "protoplast" is an isolated plant cell without a cell wall or with only parts of the cell wall.

"Regulatory elements" refer to sequences involved in controlling the expression of a nucleotide sequence. Regulatory elements comprise a promoter operably linked to the nucleotide sequence of interest and termination signals. They also typically encompass sequences required for proper translation of the nucleotide sequence.

In its broadest sense, the term "substantially similar", when used herein with respect to a nucleotide sequence, means a nucleotide sequence corresponding to a reference nucleotide sequence, wherein the corresponding sequence encodes a polypeptide having substantially the same structure and function as the polypeptide encoded by the reference nucleotide sequence, e.g. where only changes in amino acids not affecting the polypeptide function occur. Desirably the substantially similar nucleotide sequence encodes the polypeptide encoded by the reference nucleotide sequence. The percentage of identity between the substantially similar nucleotide sequence and the reference nucleotide sequence desirably is at least 80%, more desirably at least 85%, preferably at least 90%, more preferably at least 95%, still more preferably at least 99%. A nucleotide sequence

"substantially similar" to reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

"Synthetic" refers to a nucleotide sequence comprising structural characters that are not present in the natural sequence. For example, an artificial sequence that resembles more closely the G+C content and the normal codon distribution of dicot and/or monocot genes is said to be synthetic.

"Transformation" is a process for introducing heterologous nucleic acid into a host cell or organism. In particular, "transformation" means the stable integration of a DNA molecule into the genome of an organism of interest.

"Transformed / transgenic / recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof. A "non-transformed", "non-transgenic", or "non-recombinant" host refers to a wild-type organism, e.g., a bacterium or plant, which does not contain the heterologous nucleic acid molecule.

Nucleotides are indicated by their bases by the following standard abbreviations: adenine (A), cytosine (C), thymine (T), and guanine (G). Amino acids are likewise indicated by the following standard abbreviations: alanine (Ala; A), arginine (Arg; R), asparagine (Asn; N), aspartic acid (Asp; D), cysteine (Cys; C), glutamine (Gln; Q), glutamic acid (Glu; E), glycine (Gly; G), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V). Furthermore, (Xaa; X) represents any amino acid.

BRIEF DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

SEQ ID NO:1 is the sequence of the approximately 9.7 kb DNA fragment comprised in pCIB9359-7 which comprises the following ORFs at the specified nucleotide positions:

<u>Name</u>	<u>Start</u>	<u>End</u>
orf1	412	1665
orf2	1686	2447
orf3	2758	3318
orf4	3342	4118
orf5	4515	9269

SEQ ID NO:2 is the sequence of the ~46.4 kDa protein encoded by orf1 of SEQ ID NO:1.

SEQ ID NO:3 is the sequence of the ~28.1 kDa protein encoded by orf2 of SEQ ID NO:1.

SEQ ID NO:4 is the sequence of the ~20.7 kDa protein encoded by orf3 of SEQ ID NO:1.

SEQ ID NO:5 is the sequence of the ~28.7 kDa protein encoded by orf4 of SEQ ID NO:1.

SEQ ID NO:6 is the sequence of the ~176 kDa protein encoded by orf5 of SEQ ID NO:1.

SEQ ID NOs:7-10 are oligonucleotides.

SEQ ID NO:11 is the sequence of the approximately 38 kb DNA fragment comprised in pNOV2400, which comprises the following ORFs at the specified nucleotide positions (descending numbers and "C" indicates that the ORF is on the complementary strand):

<u>Name</u>	<u>Start</u>	<u>End</u>	
orf7	66	1898	(partial sequence)
hph3	2416	9909	
orf18	3395	2817	C
orf4	9966	14,633	
orf19	14,699	15,007	
orf5	15,171	18,035	
orf22	17,398	17,072	C
orf10	19,167	18,235	C
orf14	20,116	19,385	C
orf13	20,963	20,217	C
orf11	23,086	22,172	C
hph2	23,768	31,336	
orf2	31,393	35,838	

orf21	35,709	35,383	C
orf16	36,661	36,032	C
orf8	37,781	36,654	C

SEQ ID NO:11 also includes the following restriction sites, some of which are used in the subcloning steps set forth in Example 17:

<u>Restriction Site</u>	<u>Nucleotide Position(s)</u>
<i>AcdII</i>	2835
<i>BamHI</i>	18,915
<i>BsmBI</i>	11,350
<i>BstI</i> 107I	29,684
<i>EagI</i>	13,590; 31,481
<i>Eco72I</i>	34,474
<i>MluI</i>	2444; 5116; 9327; 26,204
<i>NotI</i>	13,589
<i>PacI</i>	9915; 23,353; 37,888
<i>PvuI</i>	8816
<i>SapI</i>	35,248
<i>SexAI</i>	28,946
<i>SgfI</i>	8815
<i>SpeI</i>	2157; 3769; 7831; 11,168
<i>SphI</i>	755
<i>StuI</i>	35,690
<i>Tth111I</i>	21,443

SEQ ID NO:12 is the sequence of the protein encoded by orf5 of SEQ ID NO:11.

SEQ ID NO:13 is the sequence of the protein encoded by hph2 of SEQ ID NO:11.

SEQ ID NO:14 is the sequence of the protein encoded by orf2 of SEQ ID NO:11.

SEQ ID NOs:15-22 are oligonucleotides.

DEPOSITS

The following material has been deposited with the Agricultural Research Service, Patent Culture Collection (NRRL), 1815 North University Street, Peoria, Illinois 61604, under the terms of the Budapest Treaty on the International Recognition of the Deposit of

Microorganisms for the Purposes of Patent Procedure. All restrictions on the availability of the deposited material will be irrevocably removed upon the granting of a patent.

<u>Clone</u>	<u>Accession Number</u>	<u>Date of Deposit</u>
pCIB9359-7	NRRL B-21835	September 17, 1997
pNOV2400	NRRL B-30077	December 3, 1998
pNOV1001	NRRL B-30078	December 3, 1998

Novel Nucleic Acid Sequences whose Expression Results in Insecticidal Toxins

This invention relates to nucleic acid sequences whose expression results in novel toxins, and to the making and using of the toxins to control insect pests. The nucleic acid sequences are derived from *Photorhabdus luminescens*, a member of the *Enterobacteriaceae* family. *P. luminescens* is a symbiotic bacterium of nematodes of the genus *Heterorhabditis*. The nematodes colonize insect larva, kill them, and their offspring feed on the dead larvae. The insecticidal activity is actually produced by the symbiotic *P. luminescens* bacteria. The inventors are the first to isolate the nucleic acid sequences of the present invention from *P. luminescens* (ATCC strain number 29999). The expression of the nucleic acid sequences of the present invention results in toxins that can be used to control Lepidopteran insects such as *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Manduca sexta* (Tobacco Hornworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm), as well as Coleopteran insects such as *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), *Diabrotica longicornis barberi* (Northern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

In one preferred embodiment, the invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence substantially similar to the approximately 9.7 kb nucleic acid sequence set forth in SEQ ID NO:1, whose expression results in insect control activity (further illustrated in Examples 1-11). Five open reading frames (ORFs) are present in the nucleic acid sequence set forth in SEQ ID NO:1, coding for proteins of predicted sizes 45 kDa, 28 kDa, 21 kDa, 29 kDa, and 176 kDa. The five ORFs are arranged in an operon-like structure. When expressed in a heterologous host, the ~ 9.7 kb DNA fragment from *P.*

luminescens results in insect control activity against Lepidopterans such as *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm), showing that expression of the ~ 9.7 kb nucleotide sequence set forth in SEQ ID NO:1 is necessary and sufficient for such insect control activity. In a preferred embodiment, the invention encompasses a DNA molecule, whose expression results in an insecticidal toxin, which is deposited in the *E. coli* strain pCIB9359-7 (NRRL accession number B-21835).

In another preferred embodiment, the invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence substantially similar to the approximately 38 kb nucleic acid fragment set forth in SEQ ID NO:11 and deposited in the *E. coli* strain pNOV2400 (NRRL accession number B-30077), whose expression results in insect control activity (see Examples 12-18). In a more preferred embodiment, the invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence substantially similar to the ~ 22 kb DNA fragment deposited in the *E. coli* strain pNOV1001 (NRRL accession number B-30078), whose expression results in insect control activity. In a most preferred embodiment, the invention encompasses isolated nucleic acid molecules comprising nucleotide sequences substantially similar to the three ORFs corresponding to nucleotides 23,768-31,336 (hph2), 31,393-35,838 (orf2), and 15,171-18,035 (orf5) of the DNA fragment set forth in SEQ ID NO:11, as well as the proteins encoded thereby. When co-expressed in a heterologous host, these three ORFs result in insect control activity against Lepidopterans such as *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), as well as against Coleopterans such as *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle), showing that co-expression of these three ORFs (hph2, orf2, and orf5) is necessary and sufficient for such insect control activity.

The present invention also encompasses recombinant vectors comprising the nucleic acid sequences of this invention. In such vectors, the nucleic acid sequences are preferably comprised in expression cassettes comprising regulatory elements for expression of the nucleotide sequences in a host cell capable of expressing the nucleotide sequences. Such regulatory elements usually comprise promoter and termination signals and preferably also

comprise elements allowing efficient translation of polypeptides encoded by the nucleic acid sequences of the present invention. Vectors comprising the nucleic acid sequences are usually capable of replication in particular host cells, preferably as extrachromosomal molecules, and are therefore used to amplify the nucleic acid sequences of this invention in the host cells. In one embodiment, host cells for such vectors are microorganisms, such as bacteria, in particular *E.coli*. In another embodiment, host cells for such recombinant vectors are endophytes or epiphytes. A preferred host cell for such vectors is a eukaryotic cell, such as a yeast, a plant cell, or an insect cell. Plant cells such as maize cells are most preferred host cells. In another preferred embodiment, such vectors are viral vectors and are used for replication of the nucleotide sequences in particular host cells, e.g. insect cells or plant cells. Recombinant vectors are also used for transformation of the nucleotide sequences of this invention into host cells, whereby the nucleotide sequences are stably integrated into the DNA of such host cells. In one, such host cells are prokaryotic cells. In a preferred embodiment, such host cells are eukaryotic cells, such as yeast cells, insect cells, or plant cells. In a most preferred embodiment, the host cells are plant cells, such as maize cells.

In preferred embodiments, the insecticidal toxins of the invention each comprise at least one polypeptide encoded by a nucleotide sequence of the invention. In another preferred embodiment, the insecticidal toxins are produced from a purified strain of *P. luminescens*, such the strain with ATTC accession number 29999. The toxins of the present invention have insect control activity when tested against insect pests in bioassays; and these properties of the insecticidal toxins are further illustrated in Examples 1-18. The insecticidal toxins described in the present invention are further characterized in that their molecular weights are larger than 6,000, as found by size fractionation experiments. The insecticidal toxins retain full insecticidal activity after being stored at 4°C for 2 weeks. One is also shown to retain its full insecticidal activity after being freeze-dried and stored at 22°C for 2 weeks. However, the insecticidal toxins of the invention lose their insecticidal activity after incubation for 5 minutes at 100°C.

In further embodiments, the nucleotide sequences of the invention can be modified by incorporation of random mutations in a technique known as *in-vitro* recombination or DNA shuffling. This technique is described in Stemmer et al., Nature 370: 389-391 (1994) and US Patent 5,605,793, which are incorporated herein by reference. Millions of mutant copies of a nucleotide sequence are produced based on an original nucleotide sequence of

this invention and variants with improved properties, such as increased insecticidal activity, enhanced stability, or different specificity or range of target insect pests are recovered. The method encompasses forming a mutagenized double-stranded polynucleotide from a template double-stranded polynucleotide comprising a nucleotide sequence of this invention, wherein the template double-stranded polynucleotide has been cleaved into double-stranded-random fragments of a desired size, and comprises the steps of adding to the resultant population of double-stranded random fragments one or more single or double-stranded oligonucleotides, wherein said oligonucleotides comprise an area of identity and an area of heterology to the double-stranded template polynucleotide; denaturing the resultant mixture of double-stranded random fragments and oligonucleotides into single-stranded fragments; incubating the resultant population of single-stranded fragments with a polymerase under conditions which result in the annealing of said single-stranded fragments at said areas of identity to form pairs of annealed fragments, said areas of identity being sufficient for one member of a pair to prime replication of the other, thereby forming a mutagenized double-stranded polynucleotide; and repeating the second and third steps for at least two further cycles, wherein the resultant mixture in the second step of a further cycle includes the mutagenized double-stranded polynucleotide from the third step of the previous cycle, and the further cycle forms a further mutagenized double-stranded polynucleotide. In a preferred embodiment, the concentration of a single species of double-stranded random fragment in the population of double-stranded random fragments is less than 1% by weight of the total DNA. In a further preferred embodiment, the template double-stranded polynucleotide comprises at least about 100 species of polynucleotides. In another preferred embodiment, the size of the double-stranded random fragments is from about 5 bp to 5 kb. In a further preferred embodiment, the fourth step of the method comprises repeating the second and the third steps for at least 10 cycles.

Expression of the Nucleotide Sequences in Heterologous Microbial Hosts

As biological insect control agents, the insecticidal toxins are produced by expression of the nucleotide sequences in heterologous host cells capable of expressing the nucleotide sequences. In a first embodiment, *P. luminescens* cells comprising modifications of at least one nucleotide sequence of this invention at its chromosomal location are described. Such modifications encompass mutations or deletions of existing regulatory elements, thus leading to altered expression of the nucleotide sequence, or the incorporation of new regulatory elements controlling the expression of the nucleotide sequence. In another

embodiment, additional copies of one or more of the nucleotide sequences are added to *P. luminescens* cells either by insertion into the chromosome or by introduction of extrachromosomally replicating molecules containing the nucleotide sequences.

In another embodiment, at least one of the nucleotide sequences of the invention is inserted into an appropriate expression cassette, comprising a promoter and termination signals. Expression of the nucleotide sequence is constitutive, or an inducible promoter responding to various types of stimuli to initiate transcription is used. In a preferred embodiment, the cell in which the toxin is expressed is a microorganism, such as a virus, a bacteria, or a fungus. In a preferred embodiment, a virus, such as a baculovirus, contains a nucleotide sequence of the invention in its genome and expresses large amounts of the corresponding insecticidal toxin after infection of appropriate eukaryotic cells that are suitable for virus replication and expression of the nucleotide sequence. The insecticidal toxin thus produced is used as an insecticidal agent. Alternatively, baculoviruses engineered to include the nucleotide sequence are used to infect insects *in-vivo* and kill them either by expression of the insecticidal toxin or by a combination of viral infection and expression of the insecticidal toxin.

Bacterial cells are also hosts for the expression of the nucleotide sequences of the invention. In a preferred embodiment, non-pathogenic symbiotic bacteria, which are able to live and replicate within plant tissues, so-called endophytes, or non-pathogenic symbiotic bacteria, which are capable of colonizing the phyllosphere or the rhizosphere, so-called epiphytes, are used. Such bacteria include bacteria of the genera *Agrobacterium*, *Alcaligenes*, *Azospirillum*, *Azotobacter*, *Bacillus*, *Clavibacter*, *Enterobacter*, *Erwinia*, *Flavobacter*, *Klebsiella*, *Pseudomonas*, *Rhizobium*, *Serratia*, *Streptomyces* and *Xanthomonas*. Symbiotic fungi, such as *Trichoderma* and *Gliocladium* are also possible hosts for expression of the inventive nucleotide sequences for the same purpose.

Techniques for these genetic manipulations are specific for the different available hosts and are known in the art. For example, the expression vectors pKK223-3 and pKK223-2 can be used to express heterologous genes in *E. coli*, either in transcriptional or translational fusion, behind the *tac* or *trc* promoter. For the expression of operons encoding multiple ORFs, the simplest procedure is to insert the operon into a vector such as pKK223-3 in transcriptional fusion, allowing the cognate ribosome binding site of the heterologous genes to be used. Techniques for overexpression in gram-positive species such as *Bacillus* are also known in the art and can be used in the context of this invention (Quax *et al. In.*:

Industrial Microorganisms: Basic and Applied Molecular Genetics, Eds. Baltz *et al.*, American Society for Microbiology, Washington (1993)). Alternate systems for overexpression rely for example, on yeast vectors and include the use of *Pichia*, *Saccharomyces* and *Kluyveromyces* (Sreekrishna, *In: Industrial microorganisms: basic and applied molecular genetics*, Baltz, Hegeman, and Skatrud *eds.*, American Society for Microbiology, Washington (1993); Dequin & Barre, *Biotechnology* 12:173-177 (1994); van den Berg *et al.*, *Biotechnology* 8:135-139 (1990)).

In another preferred embodiment, at least one of the described nucleotide sequences is transferred to and expressed in *Pseudomonas fluorescens* strain CGA267356 (described in the published application EU 0 472 494 and in WO 94/01561) which has biocontrol characteristics. In another preferred embodiment, a nucleotide sequence of the invention is transferred to *Pseudomonas aureofaciens* strain 30-84 which also has biocontrol characteristics. Expression in heterologous biocontrol strains requires the selection of vectors appropriate for replication in the chosen host and a suitable choice of promoter. Techniques are well known in the art for expression in gram-negative and gram-positive bacteria and fungi.

Expression of the Nucleotide Sequences in Plant Tissue

In a particularly preferred embodiment, at least one of the insecticidal toxins of the invention is expressed in a higher organism, e.g., a plant. In this case, transgenic plants expressing effective amounts of the toxins protect themselves from insect pests. When the insect starts feeding on such a transgenic plant, it also ingests the expressed toxins. This will deter the insect from further biting into the plant tissue or may even harm or kill the insect. A nucleotide sequence of the present invention is inserted into an expression cassette, which is then preferably stably integrated in the genome of said plant. In another preferred embodiment, the nucleotide sequence is included in a non-pathogenic self-replicating virus. Plants transformed in accordance with the present invention may be monocots or dicots and include, but are not limited to, maize, wheat, barley, rye, sweet potato, bean, pea, chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic, pepper, celery, squash, pumpkin, hemp, zucchini, apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot, strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya, mango, banana, soybean, tomato, sorghum, sugarcane, sugarbeet, sunflower, rapeseed, clover, tobacco, carrot, cotton, alfalfa, rice,

potato, eggplant, cucumber, *Arabidopsis*, and woody plants such as coniferous and deciduous trees.

Once a desired nucleotide sequence has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques.

A nucleotide sequence of this invention is preferably expressed in transgenic plants, thus causing the biosynthesis of the corresponding toxin in the transgenic plants. In this way, transgenic plants with enhanced resistance to insects are generated. For their expression in transgenic plants, the nucleotide sequences of the invention may require modification and optimization. Although in many cases genes from microbial organisms can be expressed in plants at high levels without modification, low expression in transgenic plants may result from microbial nucleotide sequences having codons that are not preferred in plants. It is known in the art that all organisms have specific preferences for codon usage, and the codons of the nucleotide sequences described in this invention can be changed to conform with plant preferences, while maintaining the amino acids encoded thereby. Furthermore, high expression in plants is best achieved from coding sequences that have at least 35% about GC content, preferably more than about 45%, more preferably more than about 50%, and most preferably more than about 60%. Microbial nucleotide sequences which have low GC contents may express poorly in plants due to the existence of ATTTA motifs which may destabilize messages, and AATAAA motifs which may cause inappropriate polyadenylation. Although preferred gene sequences may be adequately expressed in both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledons or dicotyledons as these preferences have been shown to differ (Murray *et al.* Nucl. Acids Res. 17: 477-498 (1989)). In addition, the nucleotide sequences are screened for the existence of illegitimate splice sites that may cause message truncation. All changes required to be made within the nucleotide sequences such as those described above are made using well known techniques of site directed mutagenesis, PCR, and synthetic gene construction using the methods described in the published patent applications EP 0 385 962 (to Monsanto), EP 0 359 472 (to Lubrizol, and WO 93/07278 (to Ciba-Geigy).

For efficient initiation of translation, sequences adjacent to the initiating methionine may require modification. For example, they can be modified by the inclusion of sequences known to be effective in plants. Joshi has suggested an appropriate consensus for plants

(NAR 15: 6643-6653 (1987)) and Clontech suggests a further consensus translation initiator (1993/1994 catalog, page 210). These consensus sequences are suitable for use with the nucleotide sequences of this invention. The sequences are incorporated into constructions comprising the nucleotide sequences, up to and including the ATG (whilst leaving the second amino acid unmodified), or alternatively up to and including the GTC subsequent to the ATG (with the possibility of modifying the second amino acid of the transgene).

Expression of the nucleotide sequences in transgenic plants is driven by promoters shown to be functional in plants. The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. Thus, expression of the nucleotide sequences of this invention in leaves, in ears, in inflorescences (*e.g.* spikes, panicles, cobs, *etc.*), in roots, and/or seedlings is preferred. In many cases, however, protection against more than one type of insect pest is sought, and thus expression in multiple tissues is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

Preferred promoters that are expressed constitutively include promoters from genes encoding actin or ubiquitin and the CaMV 35S and 19S promoters. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the insecticidal toxins to be synthesized only when the crop plants are treated with the inducing chemicals. Preferred technology for chemical induction of gene expression is detailed in the published application EP 0 332 104 (to Ciba-Geigy) and US patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

A preferred category of promoters is that which is wound inducible. Numerous promoters have been described which are expressed at wound sites and also at the sites of phytopathogen infection. Ideally, such a promoter should only be active locally at the sites of infection, and in this way the insecticidal toxins only accumulate in cells which need to synthesize the insecticidal toxins to kill the invading insect pest. Preferred promoters of this kind include those described by Stanford *et al.* Mol. Gen. Genet. 215: 200-208 (1989), Xu *et al.* Plant Molec. Biol. 22: 573-588 (1993), Logemann *et al.* Plant Cell 1: 151-158 (1989),

Rohrmeier & Lehle, *Plant Molec. Biol.* 22: 783-792 (1993), Firek *et al.* *Plant Molec. Biol.* 22: 129-142 (1993), and Warner *et al.* *Plant J.* 3: 191-201 (1993).

Preferred tissue specific expression patterns include green tissue specific, root specific, stem specific, and flower specific. Promoters suitable for expression in green tissue include many which regulate genes involved in photosynthesis and many of these have been cloned from both monocotyledons and dicotyledons. A preferred promoter is the maize PEPC promoter from the phosphoenol carboxylase gene (Hudspeth & Grula, *Plant Molec. Biol.* 12: 579-589 (1989)). A preferred promoter for root specific expression is that described by de Framond (*FEBS* 290: 103-106 (1991); EP 0 452 269 to Ciba-Geigy). A preferred stem specific promoter is that described in US patent 5,625,136 (to Ciba-Geigy) and which drives expression of the maize *trpA* gene.

Especially preferred embodiments of the invention are transgenic plants expressing at least one of the nucleotide sequences of the invention in a root-preferred or root-specific fashion. Further preferred embodiments are transgenic plants expressing the nucleotide sequences in a wound-inducible or pathogen infection-inducible manner.

In addition to the selection of a suitable promoter, constructions for expression of an insecticidal toxin in plants require an appropriate transcription terminator to be attached downstream of the heterologous nucleotide sequence. Several such terminators are available and known in the art (*e.g.* *tm1* from CaMV, E9 from *rbcS*). Any available terminator known to function in plants can be used in the context of this invention.

Numerous other sequences can be incorporated into expression cassettes described in this invention. These include sequences which have been shown to enhance expression such as intron sequences (*e.g.* from *Adh1* and *bronze1*) and viral leader sequences (*e.g.* from TMV, MCMV and AMV).

It may be preferable to target expression of the nucleotide sequences of the present invention to different cellular localizations in the plant. In some cases, localization in the cytosol may be desirable, whereas in other cases, localization in some subcellular organelle may be preferred. Subcellular localization of transgene encoded enzymes is undertaken using techniques well known in the art. Typically, the DNA encoding the target peptide from a known organelle-targeted gene product is manipulated and fused upstream of the nucleotide sequence. Many such target sequences are known for the chloroplast and their functioning in heterologous constructions has been shown. The expression of the

nucleotide sequences of the present invention is also targeted to the endoplasmic reticulum or to the vacuoles of the host cells. Techniques to achieve this are well-known in the art.

Vectors suitable for plant transformation are described elsewhere in this specification. For *Agrobacterium*-mediated transformation, binary vectors or vectors carrying at least one T-DNA border sequence are suitable, whereas for direct gene transfer any vector is suitable and linear DNA containing only the construction of interest may be preferred. In the case of direct gene transfer, transformation with a single DNA species or co-transformation can be used (Schocher *et al.* *Biotechnology* 4: 1093-1096 (1986)). For both direct gene transfer and *Agrobacterium*-mediated transfer, transformation is usually (but not necessarily) undertaken with a selectable marker which may provide resistance to an antibiotic (kanamycin, hygromycin or methotrexate) or a herbicide (basta). The choice of selectable marker is not, however, critical to the invention.

In another preferred embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. A major advantage of plastid transformation is that plastids are generally capable of expressing bacterial genes without substantial modification, and plastids are capable of expressing multiple open reading frames under control of a single promoter. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91, 7301-7305. The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate homologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab, Z., Hajdukiewicz, P., and Maliga, P. (1990) *Proc. Natl. Acad. Sci. USA* 87, 8526-8530; Staub, J. M., and Maliga, P. (1992) *Plant Cell* 4, 39-45). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub, J.M., and Maliga, P. (1993) *EMBO J.* 12, 601-606). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial

aadA gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab, Z., and Maliga, P. (1993) *Proc. Natl. Acad. Sci. USA* 90, 913-917). Previously, this marker had been used successfully for high-frequency transformation of the plastid genome of the green alga *Chlamydomonas reinhardtii* (Goldschmidt-Clermont, M. (1991) *Nucl. Acids Res.* 19: 4083-4089). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a homoplastic state. Plastid expression, in which genes are inserted by homologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplastic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Formulation of Insecticidal Compositions

The invention also includes compositions comprising at least one of the insecticidal toxins of the present invention. In order to effectively control insect pests such compositions preferably contain sufficient amounts of toxin. Such amounts vary depending on the crop to be protected, on the particular pest to be targeted, and on the environmental conditions; such as humidity, temperature or type of soil. In a preferred embodiment, compositions comprising the insecticidal toxins comprise host cells expressing the toxins without additional purification. In another preferred embodiment, the cells expressing the insecticidal toxins are lyophilized prior to their use as an insecticidal agent. In another embodiment, the insecticidal toxins are engineered to be secreted from the host cells. In cases where purification of the toxins from the host cells in which they are expressed is desired, various degrees of purification of the insecticidal toxins are reached.

The present invention further embraces the preparation of compositions comprising at least one insecticidal toxin of the present invention, which is homogeneously mixed with one or more compounds or groups of compounds described herein. The present invention also relates to methods of treating plants, which comprise application of the insecticidal toxins or compositions containing the insecticidal toxins, to plants. The insecticidal toxins

can be applied to the crop area in the form of compositions or plant to be treated, simultaneously or in succession, with further compounds. These compounds can be both fertilizers or micronutrient donors or other preparations that influence plant growth. They can also be selective herbicides, insecticides, fungicides, bactericides, nematocides, molluscicides or mixtures of several of these preparations, if desired together with further carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation. Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g. natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders or fertilizers.

A preferred method of applying insecticidal toxins of the present invention is by spraying to the environment hosting the insect pest like the soil, water, or foliage of plants. The number of applications and the rate of application depend on the type and intensity of infestation by the insect pest. The insecticidal toxins can also penetrate the plant through the roots via the soil (systemic action) by impregnating the locus of the plant with a liquid composition, or by applying the compounds in solid form to the soil, e.g. in granular form (soil application). The insecticidal toxins may also be applied to seeds (coating) by impregnating the seeds either with a liquid formulation containing insecticidal toxins, or coating them with a solid formulation. In special cases, further types of application are also possible, for example, selective treatment of the plant stems or buds. The insecticidal toxins can also be provided as bait located above or below the ground.

The insecticidal toxins are used in unmodified form or, preferably, together with the adjuvants conventionally employed in the art of formulation, and are therefore formulated in known manner to emulsifiable concentrates, coatable pastes, directly sprayable or dilutable solutions, dilute emulsions, wettable powders, soluble powders, dusts, granulates, and also encapsulations, for example, in polymer substances. Like the nature of the compositions, the methods of application, such as spraying, atomizing, dusting, scattering or pouring, are chosen in accordance with the intended objectives and the prevailing circumstances.

The formulations, compositions or preparations containing the insecticidal toxins and, where appropriate, a solid or liquid adjuvant, are prepared in known manner, for example by homogeneously mixing and/or grinding the insecticidal toxins with extenders, for example solvents, solid carriers and, where appropriate, surface-active compounds (surfactants).

Suitable solvents include aromatic hydrocarbons, preferably the fractions having 8 to 12 carbon atoms, for example, xylene mixtures or substituted naphthalenes, phthalates

such as dibutyl phthalate or dioctyl phthalate, aliphatic hydrocarbons such as cyclohexane or paraffins, alcohols and glycols and their ethers and esters, such as ethanol, ethylene glycol monomethyl or monoethyl ether, ketones such as cyclohexanone, strongly polar solvents such as N-methyl-2-pyrrolidone, dimethyl sulfoxide or dimethyl formamide, as well as epoxidized vegetable oils such as epoxidized coconut oil or soybean oil or water.

The solid carriers used e.g. for dusts and dispersible powders, are normally natural mineral fillers such as calcite, talcum, kaolin, montmorillonite or attapulgite. In order to improve the physical properties it is also possible to add highly dispersed silicic acid or highly dispersed absorbent polymers. Suitable granulated adsorptive carriers are porous types, for example pumice, broken brick, sepiolite or bentonite; and suitable nonsorbent carriers are materials such as calcite or sand. In addition, a great number of pregranulated materials of inorganic or organic nature can be used, e.g. especially dolomite or pulverized plant residues.

Suitable surface-active compounds are nonionic, cationic and/or anionic surfactants having good emulsifying, dispersing and wetting properties. The term "surfactants" will also be understood as comprising mixtures of surfactants. Suitable anionic surfactants can be both water-soluble soaps and water-soluble synthetic surface-active compounds.

Suitable soaps are the alkali metal salts, alkaline earth metal salts or unsubstituted or substituted ammonium salts of higher fatty acids (chains of 10 to 22 carbon atoms), for example the sodium or potassium salts of oleic or stearic acid, or of natural fatty acid mixtures which can be obtained for example from coconut oil or tallow oil. The fatty acid methylaurin salts may also be used.

More frequently, however, so-called synthetic surfactants are used, especially fatty sulfonates, fatty sulfates, sulfonated benzimidazole derivatives or alkylarylsulfonates.

The fatty sulfonates or sulfates are usually in the form of alkali metal salts, alkaline earth metal salts or unsubstituted or substituted ammonium salts and have a 8 to 22 carbon alkyl radical which also includes the alkyl moiety of alkyl radicals, for example, the sodium or calcium salt of lignonsulfonic acid, of dodecylsulfate or of a mixture of fatty alcohol sulfates obtained from natural fatty acids. These compounds also comprise the salts of sulfuric acid esters and sulfonic acids of fatty alcohol/ethylene oxide adducts. The sulfonated benzimidazole derivatives preferably contain 2 sulfonic acid groups and one fatty acid radical containing 8 to 22 carbon atoms. Examples of alkylarylsulfonates are the sodium, calcium or triethanolamine salts of dodecylbenzenesulfonic acid, dibutyl-naphthalenesulfonic acid, or of a naphthalenesulfonic acid/formaldehyde

condensation product. Also suitable are corresponding phosphates, e.g. salts of the phosphoric acid ester of an adduct of p-nonylphenol with 4 to 14 moles of ethylene oxide.

Non-ionic surfactants are preferably polyglycol ether derivatives of aliphatic or cycloaliphatic alcohols, or saturated or unsaturated fatty acids and alkylphenols, said derivatives containing 3 to 30 glycol ether groups and 8 to 20 carbon atoms in the (aliphatic) hydrocarbon moiety and 6 to 18 carbon atoms in the alkyl moiety of the alkylphenols.

Further suitable non-ionic surfactants are the water-soluble adducts of polyethylene oxide with polypropylene glycol, ethylenediamine propylene glycol and alkylpolypropylene glycol containing 1 to 10 carbon atoms in the alkyl chain, which adducts contain 20 to 250 ethylene glycol ether groups and 10 to 100 propylene glycol ether groups. These compounds usually contain 1 to 5 ethylene glycol units per propylene glycol unit.

Representative examples of non-ionic surfactants are nonylphenolpolyethoxyethanols, castor oil polyglycol ethers, polypropylene/polyethylene oxide adducts, tributylphenoxypolyethoxyethanol, polyethylene glycol and octylphenoxyethoxyethanol. Fatty acid esters of polyoxyethylene sorbitan and polyoxyethylene sorbitan trioleate are also suitable non-ionic surfactants.

Cationic surfactants are preferably quaternary ammonium salts which have, as N-substituent, at least one C8-C22 alkyl radical and, as further substituents, lower unsubstituted or halogenated alkyl, benzyl or lower hydroxyalkyl radicals. The salts are preferably in the form of halides, methylsulfates or ethylsulfates, e.g. stearyltrimethylammonium chloride or benzyldi(2-chloroethyl)ethylammonium bromide.

The surfactants customarily employed in the art of formulation are described, for example, in "McCutcheon's Detergents and Emulsifiers Annual," MC Publishing Corp. Ringwood, New Jersey, 1979, and Sisely and Wood, "Encyclopedia of Surface Active Agents," Chemical Publishing Co., Inc. New York, 1980.

EXAMPLES

The invention will be further described by reference to the following detailed examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified. Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by Ausubel (ed.), Current Protocols in Molecular Biology, John Wiley and Sons, Inc. (1994); T. Maniatis, E. F. Fritsch and J. Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor laboratory, Cold Spring Harbor, NY (1989); and by T.J. Silhavy, M.L. Berman, and L.W. Enquist, Experiments with Gene Fusions, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984).

A. Isolation Of Nucleotide Sequences Whose Expression Results In Toxins Active Against Lepidopteran Insects

Example 1: Construction of Cosmid Library from *Photorhabdus luminescens*

Photorhabdus luminescens strain ATCC 29999 is grown in nutrient broth at 25°C for three days as described in the ATCC protocol for bioassay. The culture is grown for 24 hours for DNA isolation. Total DNA is isolated by treating freshly grown cells resuspended in 100 mM Tris pH 8, 10 mM EDTA with 2 mg/ml lysozyme for 30 minutes at 37°C. Proteinase K is added to a final concentration of 100 mg/ml, SDS is added to a final concentration of 0.5% SDS and the sample is incubated at 45°C. After the solution becomes clear and viscous, the SDS concentration is raised to 1%, and 300 mM NaCl and an equal volume of phenol-chloroform-isoamyl alcohol are added, mixed gently for 5 minutes and centrifuged at 3K. The phenol-chloroform-isoamyl alcohol extraction is repeated twice. The aqueous phase is mixed with 0.7 volumes isopropanol, and the sample is centrifuged. The pellet is washed 3 times with 70% ethanol and the nucleic acids are gently resuspended in 0.5X TE.

The DNA is treated with 0.3 units of *Sau3A* per mg DNA at 37°C for 3.5 minutes in 100 ml volume containing a total of 6 mg DNA. The reaction is then heated for 30 minutes at 65°C to inactivate the enzyme. Then 2 units of Calf Intestinal Alkaline Phosphatase are added and incubated for 30 minutes at 37°C. The sample is mixed with an equal volume of

phenol-chloroform-isoamyl alcohol and centrifuged. The aqueous phase is removed, precipitated with 0.7 volume isopropanol and centrifuged. The supernatant is transferred to a fresh tube, precipitated with ethanol, and the nucleic acids are resuspended in 0.5X TE at a concentration of 100 hg/ml.

SuperCos cosmid vector (Stratagene, La Jolla, CA) is prepared as described by the supplier utilizing the *Bam*HI cloning site. Prepared SuperCos at 100 hg/ml is ligated with the *Sau*3A digested *P.luminescens* DNA at a molar ratio of 2:1 in a 5 ml volume overnight at 6°C. The ligation mixture is packaged using Gigapack XL III (Stratagene), as described by the supplier. Packaged phages are used to infect XL-1MR (Stratagene) cells as described by the supplier. The cosmid library is plated on L-agar with 50 mg/ml kanamycin and incubated 16 hours at 37°C. 500 colonies are patched onto fresh L-kan plates at 50 colonies per plate. From the other plates the cells are washed off with L broth and mixed with 20% glycerol and frozen at -80°C.

Example 2: Insect Bioassays

Plutella xylostella bioassays are performed by aliquoting of 50 µl of the *E. coli* culture on the solid artificial *Plutella xylostella* diet (Biever and Boldt, *Annals of Entomological Society of America*, 1971; Shelton et al., *J. Ent. Sci.* 26:17). 4 ml of the diet is poured into 1 oz. clear plastic cups (Bioserve product #9051). 5 neonate *P. xylostella* from a diet adapted lab colony are placed in each diet-containing cup and then covered with a white paper lid (Bioserve product #9049). 10 larvae are assayed per concentration. Trays of cups are placed in an incubator for 3 days at 72°F with a 14:10 (hours) light:dark cycle. Then, the number of live larvae in each cup is recorded. Bioassays for other insects are performed as described for *Plutella xylostella*, but using the diet required by the insect to be tested.

The broth of *P. luminescens* undiluted and diluted 1:100 gives 100% mortality against *P. xylostella*. The broth of *P. luminescens* also gives 100% mortality against *Diabrotica virgifera virgifera*. Three clones with activity against *P. xylostella* and *Heliothis virescens* are obtained after screening 500 *E. coli* clones by insect bioassay. These cosmid clones are given the numbers pCIB9349, pCIB9350, and pCIB9351.

Exempl 3: Is lation of th Nucleotid Sequence Resp nsible for Insect Control Activity from Clones pCIB9349, pCIB9350, and pCIB9351

The three clones pCIB9349, pCIB9350 and pCIB9351 are found to be overlapping cosmids by restriction enzyme mapping. After digestion with *PacI*, clones pCIB9349 and pCIB9351 give two DNA fragments each, and pCIB9350 gives three DNA fragments. Each fragment is isolated and is self-ligated. The enzyme *PacI* does not cut the SuperCos vector; therefore, only fragments linked to it are re-isolated. The ligation mixtures are transformed into DH5 α *E. coli* cells. Isolated transformed bacterial colonies are grown in L broth with 50 μ g/ml kanamycin, and plasmid DNA is isolated by using the alkaline miniprep protocol as described in Sambrook, et al. DNA is digested with *NotI/PacI* and two clones, pCIB9355 and pCIB9356, are found by bioassay to still contain the insecticidal activity. Clone pCIB9355 is digested with *NotI* and a 17 kb and a 4 kb DNA fragment are generated. The 17 kb fragment is isolated and ligated into Bluescript vector previously cut with *NotI* and transformed into DH5 α *E. coli* cells. The isolated transformed bacterial colonies are grown as described and plasmid DNA is isolated by the alkaline miniprep protocol. A clone containing the 17 kb insert is named pCIB9359 and tested by bioassay. The results are shown in Example 5. 3 μ g of the 17 kb insert is isolated and treated with 0.3 unit of *Sau3A* per μ g DNA for 4, 6, and 8 minutes at 37°C, heated at 75°C for 15 minutes. The samples are pooled and ligated into pUC19 previously cut with *BamHI* and treated with calf intestinal alkaline phosphatase. The ligation is transformed into DH5 α cells and plated on L agar with *Xgal/Amp* as described in Sambrook et al. and grown overnight at 37°C. White colonies are picked and grown in L broth with 100 μ g/ml and plasmid DNA is isolated as previously described. DNA is digested with *EcoRI/HindIII* and novel restriction patterns are sequenced. Sequencing primers are ordered from Genosys Biotechnologies (Woodlands, TX). Sequencing is performed using the dideoxy chain-termination method. Sequencing is completed using Applied Biosystems Inc. model 377 automated DNA sequencer (Foster City, CA). Sequence is assembled using 3.0 from Gene Codes Corporation (Ann Arbor, MI).

Example 4: Subcloning of the 9.7 kb *EcoRI/XbaI* Fragment From pCIB9359

pCIB9359 is digested with *EcoRI* and *XbaI* and the DNA is run on a 0.8% Seaplaque/TBE gel. The 9.7 kb fragment (SEQ ID NO:1) is isolated and ligated into pUC19 previously digested with *EcoRI* and *XbaI*. The ligation mixture is transformed into DH5 α *E. coli* cells. Transformed bacteria are grown and plasmid DNA is isolated as previously described. The vector containing the 9.7 kb fragment in pUC19 is designated pCIB9359-7 and bioassay results are shown in Example 5.

Example 5: Bioassay Results for Cosmid Clones pCIB9359 and pCIB9359-7

Cultures of *E. coli* strains 9359 and 9359-7 containing clones pCIB9359 and pCIB9359-7, respectively, are tested for insecticidal activity against the following insects in insect bioassays:

Insects	Clones pCIB9359 and pCIB9359-7
<i>Plutella xylostella</i> (Diamondback Moth (DBM))	+++
<i>Heliothis virescens</i> (Tobacco Budworm (TBW))	++
<i>Helicoverpa zea</i> (Corn Earworm (CEW))	+++
<i>Spodoptera exigua</i> (Beet Armyworm (BAW))	+
<i>Spodoptera frugiperda</i> (Fall Armyworm (FAW))	+
<i>Trichoplusia ni</i> (Cabbage Looper (CL))	+++
<i>Ostrinia nubilalis</i> (European Corn Borer (ECB))	++
<i>Manduca sexta</i> (Tobacco Hornworm (THW))	na
<i>Diabrotica virgifera</i> (Western Corn Rootworm (WCR))	na
<i>Agrotis ipsilon</i> (Black Cutworm (BCW))	na

na = not active

+ = significant growth inhibition

++ = >40% mortality, but less than 100%

+++ = 100% mortality

The clones show insecticidal activity against *P. xylostella*, *H. virescens*, *H. zea*, *T. ni*, and *O. nubilalis*, and significant insect control activity against *S. exigua* and *S. frugiperda*.

Example 6: Identification of Active Region of pCIB9359-7 By Subcloning

Cultures of *E. coli* strains containing subclones of pCIB9359-7 are tested for insecticidal activity in insect bioassays against *P. xylostella*.

Restriction Fragment	Nucleotide Position Relative to 9.7 kb <i>EcoRI/XbaI</i> fragment (SEQ ID NO:1) from pCIB9359-7 and Size in kb		Insecticidal Activity Against <i>Plutella xylostella</i>
<i>EcoRI/XbaI</i>	1 to 9712	9.7 kb	+++
<i>EcoRV</i>	(-912) to 2309	3.2 kb	na
<i>HindIII</i>	665 to 5438	4.7 kb	na
<i>KpnI</i>	1441 to 8137	6.9 kb	na
<i>SacI/XbaI</i>	2677 to 9712	7.0 kb	na

na = not active

+ = significant growth inhibition

++ = >40% mortality, but less than 100%

+++ = 100% mortality

Example 7: Characterization of pCIB9359-7 Insect Control Activity By Titration

Dilutions of a culture of *E. coli* strain 9359-7 containing pCIB9359-7 are tested for insecticidal activity in insect bioassays. Dilutions are prepared in a culture of *E. coli* XL-1 in a total volume of 100 μ l and are transferred to diet cups with 5 insects per cup. The results show the percentage (%) of insect mortality.

μ l 9359-7 Culture	<i>Px</i>	<i>Hv</i>	<i>Hz</i>	<i>Tn</i>
100	100	72	48	100
50	100	84	68	92
25	100	52	32	100
12.5	96	52	36	68
6.25	88	20	4	32
0	36	20	24	0

Px = *P. xylostella*, *Hv* = *H. virescens*, *Hz* = *H. zea*, *Tn* = *T. ni*.

Cultures of *E. coli* 9359-7 still show substantial insecticidal activity after dilution.

Example 8: Stability of pCIB9359-7 Activity

The stability of the toxins is tested after storage for 2 weeks at different temperatures and conditions. 300 ml of Luria broth containing 100 (μ g/ml ampicillin is inoculated with *E. coli* strain 9359-7 and grown overnight at 37°C. Samples are placed in sterile 15 ml screw cap tubes and stored at 22°C and 4°C. Another sample is centrifuged; the supernatant is removed, freeze dried and stored at 22°C. The samples are stored under these conditions for 2 weeks and then a bioassay is conducted against *P. xylostella*. The freeze dried material is resuspended in the same volume as before. All samples are resuspended by vortexing.

Conditions	Results
22°C (2 weeks)	+++
4°C (2 weeks)	+++
Freeze Dried (2 weeks)	+++

na = not active; + = significant growth inhibition; ++ = >40% mortality, but less than 100%;

+++ = 100% mortality

This demonstrates that the toxins retain their activity for at least two weeks at 22°C, 4°C, and freeze-dried, and are therefore very stable.

Example 9: Size Fraction of pCIB9359-7 Activity

The approximate sizes of the insecticidal toxins are determined. *P. luminescens* cosmid clones pCIB9359-7 and pUC19 in *E. coli* host DH5 α are grown in media consisting of 50% Terrific broth and 50% Luria broth, supplemented with 50 μ g/ml ampicillin. Cultures (three tubes of each strain) are inoculated into 3 ml of the above media in culture tubes and incubated on a roller wheel overnight at 37°C. Cultures of each strain are combined and sonicated using a Branson Model 450 Sonicator, micro tip, for approximately six 10 second cycles with cooling on ice between cycles. The sonicates are centrifuged in a Sorvall SS34 rotor at 6000 RPM for 10 minutes. The resultant supernatants are filtered through a 0.2 μ filter. The 3 ml fractions of the filtrates are applied to Bio-Rad Econo-Pac 10DG columns that have been previously equilibrated with 10 ml of 50mM NaCl, 25 mM Tris base, pH 7.0. The flow through collected during sample loading is discarded. The samples are fractionated with two subsequent additions of 4 ml each of the NaCl - Tris equilibration buffer. The two four ml fractions are saved for testing. The first fraction contains all material above about 6,000 mol. wt; the second fraction contains material smaller than 6,000 mol. wt. A sample of the whole culture broth, the sonicate, and the filtered supernatant on the sonicate are tested along with the three fractions from the 10DG column for activity on *P. xylostella* neonates in bioassays.

The culture, the sonicate, and the filtered supernatant of the sonicate, and the first column fraction from the 9359-7 sample are highly active on *P. xylostella*. The second column fraction from 9359-7 is slightly active (some stunting only). No activity is found in the third fraction from 9359-7. The sample from DH5-pUC19 does not have any activity. This indicates that the molecular weights of the toxins are above 6,000.

Example 10: Heat Inactivation of pCIB9359-7 Activity

The heat stability of the toxins is determined. Overnight cultures of the *E. coli* strain pCIB9359-7 are grown in a 50:50 mixture of Luria broth and Terrific broth. Cultures are grown at 37°C in culture tubes on a tube roller. A one ml sample of the culture is placed in

a 1.5 ml eppendorf tube and placed in a boiling water bath. The sample is removed after five minutes and allowed to cool to room temperature. This sample along with an untreated portion of the culture is assayed on *P. xylostella*. 50µl of sample of sample is spread on diet, allowed to dry and neonate larvae *P. xylostella* applied to the surface. The assay is incubated for 5 days at room temperature.

The untreated sample causes 100% mortality. The heat treated sample and a diet alone control do not cause any observable mortality, showing the toxins are heat sensitive.

Example 11: Leaf Dip Bioassay of pCIB9359-7

Insecticidal activity of the toxins is tested in a leaf dip bioassay. Six leaves approximately 2cm in diameter each are cut from seedlings of turnip and placed in a 1oz. plastic cup (Jet Plastica) with 4ml-5ml of the resuspended toxin, covered tightly, and shaken until thoroughly wetted. The treated leaves are placed in 50mm petri dishes (Gelman Sciences) on absorbent pads moistened with 300µl of water. The dish covers are left open until the leaf surface appears dry and then placed on tightly so that the leaves do not dry out.

Ten neonate *P. xylostella* larvae are placed in each petri dish arena. Also, a treatment of 0.1% Bond spreader/sticker with no toxin is set up as a control. The arenas are monitored daily for signs of drying leaves, and water is added or leaves replaced if necessary. After 3 days the leaves and arenas are examined under a dissecting microscope, and the number of live larvae in each arena is recorded.

100% mortality is found for 9359-7 and none in the no-toxin control, showing that the toxins are also insecticidal in a leaf dip assay.

B. Isolation Of Nucleic Acid Sequences Whose Expression Results In Toxins Active Against Lepidopteran and Coleopteran Insects

Example 12: Total DNA Isolation from *Photobacterium luminescens*

Photobacterium luminescens strain ATCC 29999 is grown 14-18 hours in L broth. Total DNA is isolated from 1.5 mls of culture resuspended in 0.5% SDS, 100µg/ml proteinase K, TE to a final volume of 600 µl. After a 1 hour incubation at 37°C, 100µl 5M

NaCl and 80µl CTAB/NaCl are added and the culture is incubated at 65°C for 10 minutes. An equal volume of chloroform is added; the culture is mixed gently and spun. The aqueous phase is extracted once with phenol and once with chloroform. The nucleic acids are treated with 10 µg RNase A for 30 minutes at room temperature. The aqueous phase is mixed with 0.6 volumes isopropanol and the sample is centrifuged. The pellet is washed once with 70% ethanol and the nucleic acids are gently resuspended in 100-200ul TE.

Example 13: PCR Amplification of Probes

Two probes are PCR amplified from *Photorhabdus luminescens* strain ATCC 29999 genomic DNA using oligos 5'-ACACAGCAGGTTTCGTCAG-3' (SEQ ID NO:7) and 5'-GGCAGAAGCACTCAACTC-3' (SEQ ID NO:8) to amplify probe #1 and oligos 5'-ATTGATAGCACGCGGCGACC-3' (SEQ ID NO:9) and 5'-TTGTAACGTGGAGCCGAACTGG-3' (SEQ ID NO:10) to amplify probe #2. The oligos are ordered from Genosys Biotechnologies, Inc. (Texas). Approximately 10-50 ng of genomic DNA is used as the template. 0.8µM of oligos, 200µM of dNTPs, 1X Taq DNA Polymerase buffer and 2.5 units of Taq DNA Polymerase are included in the reaction. The reaction conditions are as follows:

94°C - 1 minute

94°C - 30 seconds / 60°C - 30 seconds / 72°C - 30 seconds (25 cycles)

72°C - 5 minutes

4°C - indefinite soak

The reactions are preferably carried out in a PCR System 9600 (Perkin Elmer) thermocycler.

Example 14: Probing a *Photorhabdus luminescens* Library

600 clones from the *P. luminescens* cosmid library described in Example 1 are patched to L-amp plates in duplicate. The colonies are grown overnight then moved to 4°C. The colonies are lifted onto Colony/Plaque Screen Hybridization Transfer Membranes (Biotechnology Systems NEN Research Products). The membranes are incubated 2-3 minutes in 0.75ml 0.5N NaOH twice. The membranes are then incubated 2-3 minutes in

0.75ml 1.0M Tris-HCl, pH 7.5 twice. The membranes are allowed to dry at room temperature.

Probe #1 and probe #2 described in Example 13 are labeled using the DECAprime II Kit as described by the manufacturer (Ambion cat# 1455). Unincorporated nucleotides are removed from the labeled probes using Quick Spin Columns as described by the manufacturer (Boehringer Mannheim cat #1273973). The labeled probes are measured for incorporated radioactivity and the specific activity is 10,000,000 cpm. Membranes are prewetted with 2X SSC and hybridized with the probes for 12-16 hours at 65°C. One set of colony lifts is hybridized with probe #1 and the other set is hybridized with probe #2. The membranes are washed with wash CHURCH solutions 1 and 2 (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1984)) and exposed to Kodak film.

Twenty one clones are identified that hybridize to probe #1 and seven clones are identified that hybridize to probe #2. The gene in the clones isolated with probe #1 is named *hph1* and the gene in the clones isolated with probe #2 is named *hph2*.

Example 15: Insect Bioassays

The clones identified in Example 14 are tested for insecticidal activity against the following insects in insect bioassays: *Diabrotica virgifera virgifera* (Western Corn Rootworm (WCR)), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm (SCR)), *Ostrinia nubilalis* (European Corn Borer (ECB)), and *Plutella xylostella* (Diamondback Moth (DBM)).

Diabrotica virgifera virgifera (Western Corn Rootworm) and *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm) assays are performed using a diet incorporation method. 500µl of an overnight culture of the cosmid library in XL-1 Blue MR cells (Stratagene) is sonicated and then mixed with 500µl of diet. Once the diet solidifies, it is dispensed in a petri dish and 20 larvae are introduced over the diet. Trays of dishes are placed in an incubator for 3-5 days, and percent mortality is recorded at the end of the assay period.

Ostrinia nubilalis (European Corn Borer) and *Plutella xylostella* (Diamondback Moth) assays are performed by a surface treatment method. The diet is poured in the petri dish and allowed it to solidify. The *E. coli* culture of 200 -300µl volume is dispensed over the diet surface and entire diet surface is covered to spread the culture with the help of bacterial loop. Once the surface is dry, 10 larvae are introduced over the diet surface. Trays of

dishes are placed in an incubator for 3-5 days. The assay with European Corn Borer is incubated at 30°C in complete darkness; the assay with Diamondback Moth is incubated at 72°F with a 14:10 (hours) light:dark cycle. Percent mortality is recorded at the end of the assay period.

Cosmids containing *hph2* are identified with a range of activities, including: WCR only; SCR only; WCR and SCR; SCR and ECB; WCR, SCR, and ECB; or WCR, SCR, ECB, and DBM activity.

In addition to probing the *P. luminescens* cosmid library with DNA probes, 600 clones are screened by Western Corn Rootworm bioassay. A clone is identified with activity against Western Corn Rootworm. This clone hybridizes with probe #2.

From these bioassays, cosmid 514, having activity against WCR, SCR, ECB, and DBM, is selected for sequencing.

Example 16: Sequencing of Cosmid 514

Cosmid 514 is sequenced using dye terminator chemistry on an ABI 377 instrument. The nucleotide sequence of cosmid 514 is set forth as SEQ ID NO:11. Cosmid 514 is designated pNOV2400 and deposited with the NRRL in *E. coli* DH5 α and assigned accession no. B-30077.

Example 17: Subcloning Insecticidal Regions of Cosmid 514

514a

An 9011 base pair fragment within cosmid 514 (SEQ ID NO:11) is removed by digesting the cosmid with the restriction endonuclease *SpeI* (New England Biolabs (Massachusetts)), and ligating (T4 DNA Ligase, NEB) the remainder of 514. Subclone 514a consists of cosmid 514 DNA from base pairs 1-2157 ligated to base pairs 11,169-37,948.

H2O2/pET34

hph2 and *orf2* (SEQ ID NO:11, base pairs 23,768-35,838) are cloned into pET34b (Novagen, Wisconsin). Restriction sites are engineered on both ends of each gene to facilitate cloning. PCR is used to add the restriction sites to the genes. A *Bam*HI site is on the 5' end of *hph2* immediately upstream of the ATG of *hph2*, and a *SacI* site is added to

the 3' end of *hph2* immediately following the DNA triplet encoding the stop codon. A guanidine is added between the *Bam*HI site and the start codon of *hph2* to put the *hph2* gene in frame with the Cellulose Binding Domain tag in pET34b. *Orf2* has a *Sac*I site upstream of the 56 base pairs between the stop codon of *hph2* and the start codon of *orf2*. The 56 base pairs are included in the *hph2-orf2* construct to mimic their setup in the 514 cosmid. *Orf2* has an *Xho*I site on the 3' end immediately following the stop codon. The oligos used to add the restriction sites to *hph2* and *orf2* are as follows:

- hph2*-A 5'-CGGGATCCGATGATTTTAAAAGG-3' (SEQ ID NO:15)
- hph2*-B 5'-GCGCCATTGATTTGAG-3' (SEQ ID NO:16)
- hph2*-C 5'-CATTAGAGGTCGAACGTAC-3' (SEQ ID NO:17)
- hph2*-D 5'-GAGCGAGCTCTTACTTAATGGTGTAG-3' (SEQ ID NO:18)
- orf2*-A3 5'-CAGCGAGCTCCATGCAGAATTCACAGAC-3' (SEQ ID NO:19)
- orf2*-B 5'-GGCAATGGCAGCGATAAG-3' (SEQ ID NO:20)
- orf2*-C 5'-CATTAACGCAGGAAGAGC-3' (SEQ ID NO:21)
- orf2*-D 5'-GACCTCGAGTTACACGAGCGCGTCAG-3' (SEQ ID NO:22)

The *Bam*HI-*Sac*I 7583 base pair fragment, corresponding to the *hph2* gene, and the *Sac*I-*Xho*I 4502 base pair *orf2* (including the 56 base pairs between *hph2* and *orf2* open reading frames), corresponding to *orf2*, are ligated with *Bam*HI-*Xho*I-digested vector DNA pET34b.

Orf5/pBS (NotI-BamHI)

The 5325 base pair *Not*I-*Bam*HI fragment of cosmid 514 is cloned into pBS-SK using *A*fIII-*Not*I (415 bp) and *Bam*HI-*A*fIII (2530 bp) fragments of pBS-SK.

O5-H2-O2

The 12,031 base pair *Bam*HI-*Xho*I fragment of H2O2/pET34 is cloned into the 8220 base pair *Xho*I-*Bam*HI fragment of Orf5/pBS.

O51011H2O2

A 7298 base pair *Bam*HI-*M*luI fragment from subclone 514a is ligated (T4 DNA Ligase, NEB) with 9588 bp *M*luI-*Xho*I and 8220 bp *Xho*I-*Bam*HI fragments of subclone O5-H2-O2. The resulting ~ 22 kb subclone O51011H2O2, which has activity against WCR and

ECB, is designated pNOV1001 and deposited with the NRRL in *E. coli* DH5 α and assigned accession no. B-30078.

AKH2O2

A 12,074 base pair *Bam*HI-AvrII fragment of H2O2/pET34 is ligated (T4 DNA Ligase, NEB) into pK184 *Nhe*I-*Bam*HI fragment (2228 bp), generating a clone containing hph2 and orf2 in a p15a origin of replication, kanamycin-resistant vector.

Example 18: Insecticidal Activity of Subclones

Bioassays as described above are performed with *E. coli* cultures that express the above subclones, both singly and in combination. Coexpressing AKH2O2 and Orf5/pBS in *E. coli*, for example in DH5 α or HB101, is found to give insecticidal activity against the Lepidopterans *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), as well as against the Coleopterans *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle). Thus, coexpression of hph2 (SEQ ID NO:11, base pairs 23,768-31,336), orf2 (SEQ ID NO:11, base pairs 31,393-35,838), and orf5 (SEQ ID NO:11, base pairs 15,171-18,035) is sufficient to control these insects. In addition, expression of each of these three ORFs on separate plasmids gives insect control activity, demonstrating that they do not have to be genetically linked to be active, so long as all three gene products are present.

C. Expression of the Nucleic Acid Sequences of the Invention in Heterologous Microbial Hosts

Microorganisms which are suitable for the heterologous expression of the nucleotide sequences of the invention are all microorganisms which are capable of colonizing plants or the rhizosphere. As such they will be brought into contact with insect pests. These include gram-negative microorganisms such as *Pseudomonas*, *Enterobacter* and *Serratia*, the gram-positive microorganism *Bacillus* and the fungi *Trichoderma*, *Gliocladium*, and *Saccharomyces cerevisiae*. Particularly preferred heterologous hosts are *Pseudomonas fluorescens*, *Pseudomonas putida*, *Pseudomonas cepacia*, *Pseudomonas aureofaciens*,

Pseudomonas aurantiaca, *Enterobacter cloacae*, *Serratia marcescens*, *Bacillus subtilis*, *Bacillus cereus*, *Trichoderma viride*, *Trichoderma harzianum*, *Gliocladium virens*, and *Saccharomyces cerevisiae*.

Example 19: Expression of the Nucleotide Sequences in *E. coli* and Other Gram-Negative Bacteria

Many genes have been expressed in gram-negative bacteria in a heterologous manner. Expression vector pKK223-3 (Pharmacia catalogue # 27-4935-01) allows expression in *E. coli*. This vector has a strong *tac* promoter (Brosius, J. *et al.*, *Proc. Natl. Acad. Sci. USA* 81) regulated by the *lac* repressor and induced by IPTG. A number of other expression systems have been developed for use in *E. coli*. The thermoinducible expression vector pPL (Pharmacia #27-4946-01) uses a tightly regulated bacteriophage λ promoter which allows for high level expression of proteins. The *lac* promoter provides another means of expression but the promoter is not expressed at such high levels as the *tac* promoter. With the addition of broad host range replicons to some of these expression system vectors, expression of the nucleotide sequence in closely related gram negative-bacteria such as *Pseudomonas*, *Enterobacter*, *Serratia* and *Erwinia* is possible. For example, pLRKD211 (Kaiser & Kroos, *Proc. Natl. Acad. Sci. USA* 81: 5816-5820 (1984)) contains the broad host range replicon *ori T* which allows replication in many gram-negative bacteria.

In *E. coli*, induction by IPTG is required for expression of the *tac* (*i.e.* *trp-lac*) promoter. When this same promoter (*e.g.* on wide-host range plasmid pLRKD211) is introduced into *Pseudomonas* it is constitutively active without induction by IPTG. This *trp-lac* promoter can be placed in front of any gene or operon of interest for expression in *Pseudomonas* or any other closely related bacterium for the purposes of the constitutive expression of such a gene. Thus, a nucleotide sequence whose expression results in an insecticidal toxin can therefore be placed behind a strong constitutive promoter, transferred to a bacterium which has plant or rhizosphere colonizing properties turning this organism to an insecticidal agent. Other possible promoters can be used for the constitutive expression of the nucleotide sequence in gram-negative bacteria. These include, for example, the promoter from the *Pseudomonas* regulatory genes *gafA* and *lemA* (WO 94/01561) and the

Pseudomonas savastanoi IAA operon promoter (Gaffney *et al.*, *J. Bacteriol.* 172: 5593-5601 (1990)).

Example 20: Expression of the Nucleotide Sequences in Gram-Positive Bacteria

Heterologous expression of the nucleotides sequence in gram-positive bacteria is another means of producing the insecticidal toxins. Expression systems for *Bacillus* and *Streptomyces* are the best characterized. The promoter for the erythromycin resistance gene (*ermR*) from *Streptococcus pneumoniae* has been shown to be active in gram-positive aerobes and anaerobes and also in *E.coli* (Trieu-Cuot *et al.*, *Nucl Acids Res* 18: 3660 (1990)). A further antibiotic resistance promoter from the thiostreptone gene has been used in *Streptomyces* cloning vectors (Bibb, *Mol Gen Genet* 199: 26-36 (1985)). The shuttle vector pHT3101 is also appropriate for expression in *Bacillus* (Lereclus, *FEMS Microbiol Lett* 60: 211-218 (1989)). A significant advantage of this approach is that many gram-positive bacteria produce spores which can be used in formulations that produce insecticidal agents with a longer shelf life. *Bacillus* and *Streptomyces* species are aggressive colonizers of soils

Example 21: Expression of the Nucleotide Sequences in Fungi

Trichoderma harzianum and *Gliocladium virens* have been shown to provide varying levels of biocontrol in the field (US 5,165,928 and US 4,996,157, both to Cornell Research Foundation). A nucleotide sequence whose expression results in an insecticidal toxin could be expressed in such a fungus. This could be accomplished by a number of ways which are well known in the art. One is protoplast-mediated transformation of the fungus by PEG or electroporation-mediated techniques. Alternatively, particle bombardment can be used to transform protoplasts or other fungal cells with the ability to develop into regenerated mature structures. The vector pAN7-1, originally developed for *Aspergillus* transformation and now used widely for fungal transformation (Curragh *et al.*, *Mycol. Res.* 97(3): 313-317 (1992); Tooley *et al.*, *Curr. Genet.* 21: 55-60 (1992); Punt *et al.*, *Gene* 56: 117-124 (1987)) is engineered to contain the nucleotide sequence. This plasmid contains the *E. coli* the hygromycin B resistance gene flanked by the *Aspergillus nidulans* *gpd* promoter and the *trpC* terminator (Punt *et al.*, *Gene* 56: 117-124 (1987)).

In a preferred embodiment, the nucleic acid sequences of the invention are expressed in the yeast *Saccharomyces cerevisiae*. Each of the three ORF's of SEQ ID NO:11 (hph2, orf2 and orf5), which together confer insecticidal activity, are cloned into individual vectors with the GAL1 inducible promoter and the CYC1 terminator. Each vector has ampicillin resistance and the 2 micron replicon. The vectors differ in their yeast growth markers. hph2 is cloned into p424 (TRP1, ATCC 87329), orf2 into p423 (HIS3, ATCC 87327), and orf5 into p425 (LEU2, ATCC 87331). The three constructs are transformed into *S. cerevisiae* independently and together. The three ORFs are expressed together and tested for protein expression and insecticidal activity.

D. Expression of the Nucleotide Sequences in Transgenic Plants

The nucleic acid sequences described in this application can be incorporated into plant cells using conventional recombinant DNA technology. Generally, this involves inserting a coding sequence of the invention into an expression system to which the coding sequence is heterologous (i.e., not normally present) using standard cloning procedures known in the art. The vector contains the necessary elements for the transcription and translation of the inserted protein-coding sequences. A large number of vector systems known in the art can be used, such as plasmids, bacteriophage viruses and other modified viruses. Suitable vectors include, but are not limited to, viral vectors such as lambda vector systems λ gt11, λ gt10 and Charon 4; plasmid vectors such as pBI121, pBR322, pACYC177, pACYC184, pAR series, pKK223-3, pUC8, pUC9, pUC18, pUC19, pLG339, pRK290, pKC37, pKC101, pCDNAII; and other similar systems. The components of the expression system may also be modified to increase expression. For example, truncated sequences, nucleotide substitutions or other modifications may be employed. The expression systems described herein can be used to transform virtually any crop plant cell under suitable conditions. Transformed cells can be regenerated into whole plants such that the nucleotide sequence of the invention confer insect resistance to the transgenic plants.

Example 22: Modification of Coding Sequences and Adjacent Sequences

The nucleotide sequences described in this application can be modified for expression in transgenic plant hosts. A host plant expressing the nucleotide sequences and

which produces the insecticidal toxins in its cells has enhanced resistance to insect attack and is thus better equipped to withstand crop losses associated with such attack.

The transgenic expression in plants of genes derived from microbial sources may require the modification of those genes to achieve and optimize their expression in plants. In particular, bacterial ORFs which encode separate enzymes but which are encoded by the same transcript in the native microbe are best expressed in plants on separate transcripts. To achieve this, each microbial ORF is isolated individually and cloned within a cassette which provides a plant promoter sequence at the 5' end of the ORF and a plant transcriptional terminator at the 3' end of the ORF. The isolated ORF sequence preferably includes the initiating ATG codon and the terminating STOP codon but may include additional sequence beyond the initiating ATG and the STOP codon. In addition, the ORF may be truncated, but still retain the required activity; for particularly long ORFs, truncated versions which retain activity may be preferable for expression in transgenic organisms. By "plant promoter" and "plant transcriptional terminator" it is intended to mean promoters and transcriptional terminators which operate within plant cells. This includes promoters and transcription terminators which may be derived from non-plant sources such as viruses (an example is the Cauliflower Mosaic Virus).

In some cases, modification to the ORF coding sequences and adjacent sequence is not required. It is sufficient to isolate a fragment containing the ORF of interest and to insert it downstream of a plant promoter. For example, Gaffney *et al.* (Science 261: 754-756 (1993)) have expressed the *Pseudomonas nahG* gene in transgenic plants under the control of the CaMV 35S promoter and the CaMV *tml* terminator successfully without modification of the coding sequence and with x bp of the *Pseudomonas* gene upstream of the ATG still attached, and y bp downstream of the STOP codon still attached to the *nahG* ORF. Preferably as little adjacent microbial sequence should be left attached upstream of the ATG and downstream of the STOP codon. In practice, such construction may depend on the availability of restriction sites.

In other cases, the expression of genes derived from microbial sources may provide problems in expression. These problems have been well characterized in the art and are particularly common with genes derived from certain sources such as *Bacillus*. These problems may apply to the nucleotide sequence of this invention and the modification of these genes can be undertaken using techniques now well known in the art. The following problems may be encountered:

1. Codon Usage.

The preferred codon usage in plants differs from the preferred codon usage in certain microorganisms. Comparison of the usage of codons within a cloned microbial ORF to usage in plant genes (and in particular genes from the target plant) will enable an identification of the codons within the ORF which should preferably be changed. Typically plant evolution has tended towards a strong preference of the nucleotides C and G in the third base position of monocotyledons, whereas dicotyledons often use the nucleotides A or T at this position. By modifying a gene to incorporate preferred codon usage for a particular target transgenic species, many of the problems described below for GC/AT content and illegitimate splicing will be overcome.

2. GC/AT Content.

Plant genes typically have a GC content of more than 35%. ORF sequences which are rich in A and T nucleotides can cause several problems in plants. Firstly, motifs of ATTTA are believed to cause destabilization of messages and are found at the 3' end of many short-lived mRNAs. Secondly, the occurrence of polyadenylation signals such as AATAAA at inappropriate positions within the message is believed to cause premature truncation of transcription. In addition, monocotyledons may recognize AT-rich sequences as splice sites (see below).

3. Sequences Adjacent to the Initiating Methionine.

Plants differ from microorganisms in that their messages do not possess a defined ribosome binding site. Rather, it is believed that ribosomes attach to the 5' end of the message and scan for the first available ATG at which to start translation. Nevertheless, it is believed that there is a preference for certain nucleotides adjacent to the ATG and that expression of microbial genes can be enhanced by the inclusion of a eukaryotic consensus translation initiator at the ATG. Clontech (1993/1994 catalog, page 210, incorporated herein by reference) have suggested one sequence as a consensus translation initiator for the expression of the *E. coli uidA* gene in plants. Further, Joshi (NAR 15: 6643-6653 (1987), incorporated herein by reference) has compared many plant sequences adjacent to the ATG and suggests another consensus sequence. In situations where difficulties are encountered in the expression of microbial ORFs in plants, inclusion of one of these sequences at the initiating ATG may improve translation. In such cases the last three

nucleotides of the consensus may not be appropriate for inclusion in the modified sequence due to their modification of the second AA residue. Preferred sequences adjacent to the initiating methionine may differ between different plant species. A survey of 14 maize genes located in the GenBank database provided the following results:

Position Before the Initiating ATG in 14 Maize Genes:

	<u>-10</u>	<u>-9</u>	<u>-8</u>	<u>-7</u>	<u>-6</u>	<u>-5</u>	<u>-4</u>	<u>-3</u>	<u>-2</u>	<u>-1</u>
C	3	8	4	6	2	5	6	0	10	7
T	3	0	3	4	3	2	1	1	1	0
A	2	3	1	4	3	2	3	7	2	3
G	6	3	6	0	6	5	4	6	1	5

This analysis can be done for the desired plant species into which the nucleotide sequence is being incorporated, and the sequence adjacent to the ATG modified to incorporate the preferred nucleotides.

4. Removal of Illegitimate Splice Sites.

Genes cloned from non-plant sources and not optimized for expression in plants may also contain motifs which may be recognized in plants as 5' or 3' splice sites, and be cleaved, thus generating truncated or deleted messages. These sites can be removed using the techniques well known in the art.

Techniques for the modification of coding sequences and adjacent sequences are well known in the art. In cases where the initial expression of a microbial ORF is low and it is deemed appropriate to make alterations to the sequence as described above, then the construction of synthetic genes can be accomplished according to methods well known in the art. These are, for example, described in the published patent disclosures EP 0 385 962 (to Monsanto), EP 0 359 472 (to Lubrizol) and WO 93/07278 (to Ciba-Geigy), all of which are incorporated herein by reference. In most cases it is preferable to assay the expression of gene constructions using transient assay protocols (which are well known in the art) prior to their transfer to transgenic plants.

Example 23: Construction of Plant Expression Cassettes

Coding sequences intended for expression in transgenic plants are first assembled in expression cassettes behind a suitable promoter expressible in plants. The expression cassettes may also comprise any further sequences required or selected for the expression of the transgene. Such sequences include, but are not restricted to, transcription terminators, extraneous sequences to enhance expression such as introns, vital sequences, and sequences intended for the targeting of the gene product to specific organelles and cell compartments. These expression cassettes can then be easily transferred to the plant transformation vectors described below. The following is a description of various components of typical expression cassettes.

1. Promoters

The selection of the promoter used in expression cassettes will determine the spatial and temporal expression pattern of the transgene in the transgenic plant. Selected promoters will express transgenes in specific cell types (such as leaf epidermal cells, mesophyll cells, root cortex cells) or in specific tissues or organs (roots, leaves or flowers, for example) and the selection will reflect the desired location of accumulation of the gene product. Alternatively, the selected promoter may drive expression of the gene under various inducing conditions. Promoters vary in their strength, i.e., ability to promote transcription. Depending upon the host cell system utilized, any one of a number of suitable promoters can be used, including the gene's native promoter. The following are non-limiting examples of promoters that may be used in expression cassettes.

a. Constitutive Expression, the Ubiquitin Promoter:

Ubiquitin is a gene product known to accumulate in many cell types and its promoter has been cloned from several species for use in transgenic plants (e.g. sunflower - Binet *et al.* *Plant Science* **79**: 87-94 (1991); maize - Christensen *et al.* *Plant Molec. Biol.* **12**: 619-632 (1989); and *Arabidopsis* - Norris *et al.*, *Plant Mol. Biol.* **21**:895-906 (1993)). The maize ubiquitin promoter has been developed in transgenic monocot systems and its sequence and vectors constructed for monocot transformation are disclosed in the patent publication EP 0 342 926 (to Lubrizol) which is herein incorporated by reference. Taylor *et al.* (*Plant Cell Rep.* **12**: 491-495 (1993)) describe a vector (pAHC25) that comprises the maize ubiquitin promoter and first intron and its high activity in cell suspensions of numerous

monocotyledons when introduced via microprojectile bombardment. The *Arabidopsis* ubiquitin promoter is ideal for use with the nucleotide sequences of the present invention. The ubiquitin promoter is suitable for gene expression in transgenic plants, both monocotyledons and dicotyledons. Suitable vectors are derivatives of pAHC25 or any of the transformation vectors described in this application, modified by the introduction of the appropriate ubiquitin promoter and/or intron sequences.

b. Constitutive Expression, the CaMV 35S Promoter:

Construction of the plasmid pCGN1761 is described in the published patent application EP 0 392 225 (Example 23), which is hereby incorporated by reference. pCGN1761 contains the "double" CaMV 35S promoter and the *tm1* transcriptional terminator with a unique *EcoRI* site between the promoter and the terminator and has a pUC-type backbone. A derivative of pCGN1761 is constructed which has a modified polylinker which includes *NotI* and *XhoI* sites in addition to the existing *EcoRI* site. This derivative is designated pCGN1761ENX. pCGN1761ENX is useful for the cloning of cDNA sequences or coding sequences (including microbial ORF sequences) within its polylinker for the purpose of their expression under the control of the 35S promoter in transgenic plants. The entire 35S promoter-coding sequence-*tm1* terminator cassette of such a construction can be excised by *HindIII*, *SphI*, *Sall*, and *XbaI* sites 5' to the promoter and *XbaI*, *BamHI* and *BglII* sites 3' to the terminator for transfer to transformation vectors such as those described below. Furthermore, the double 35S promoter fragment can be removed by 5' excision with *HindIII*, *SphI*, *Sall*, *XbaI*, or *PstI*, and 3' excision with any of the polylinker restriction sites (*EcoRI*, *NotI* or *XhoI*) for replacement with another promoter. If desired, modifications around the cloning sites can be made by the introduction of sequences that may enhance translation. This is particularly useful when overexpression is desired. For example, pCGN1761ENX may be modified by optimization of the translational initiation site as described in Example 37 of U.S. Patent No. 5,639,949, incorporated herein by reference.

c. Constitutive Expression, the Actin Promoter:

Several isoforms of actin are known to be expressed in most cell types and consequently the actin promoter is a good choice for a constitutive promoter. In particular, the promoter from the rice *Act1* gene has been cloned and characterized (McElroy *et al.* Plant Cell 2: 163-171 (1990)). A 1.3kb fragment of the promoter was found to contain all

the regulatory elements required for expression in rice protoplasts. Furthermore, numerous expression vectors based on the *Act1* promoter have been constructed specifically for use in monocotyledons (McElroy *et al.* Mol. Gen. Genet. 231: 150-160 (1991)). These incorporate the *Act1*-intron 1, *Adh1* 5' flanking sequence and *Adh1*-intron 1 (from the maize alcohol dehydrogenase gene) and sequence from the CaMV 35S promoter. Vectors showing highest expression were fusions of 35S and *Act1* intron or the *Act1* 5' flanking sequence and the *Act1* intron. Optimization of sequences around the initiating ATG (of the GUS reporter gene) also enhanced expression. The promoter expression cassettes described by McElroy *et al.* (Mol. Gen. Genet. 231: 150-160 (1991)) can be easily modified for gene expression and are particularly suitable for use in monocotyledonous hosts. For example, promoter-containing fragments is removed from the McElroy constructions and used to replace the double 35S promoter in pCGN1761ENX, which is then available for the insertion of specific gene sequences. The fusion genes thus constructed can then be transferred to appropriate transformation vectors. In a separate report, the rice *Act1* promoter with its first intron has also been found to direct high expression in cultured barley cells (Chibbar *et al.* Plant Cell Rep. 12: 506-509 (1993)).

d. Inducible Expression, the PR-1 Promoter:

The double 35S promoter in pCGN1761ENX may be replaced with any other promoter of choice that will result in suitably high expression levels. By way of example, one of the chemically regulatable promoters described in U.S. Patent No. 5,614,395 may replace the double 35S promoter. The promoter of choice is preferably excised from its source by restriction enzymes, but can alternatively be PCR-amplified using primers that carry appropriate terminal restriction sites. Should PCR-amplification be undertaken, then the promoter should be re-sequenced to check for amplification errors after the cloning of the amplified promoter in the target vector. The chemically/pathogen regulatable tobacco PR-1a promoter is cleaved from plasmid pCIB1004 (for construction, see example 21 of EP 0 332 104, which is hereby incorporated by reference) and transferred to plasmid pCGN1761ENX (Uknes *et al.*, 1992). pCIB1004 is cleaved with *NcoI* and the resultant 3' overhang of the linearized fragment is rendered blunt by treatment with T4 DNA polymerase. The fragment is then cleaved with *HindIII* and the resultant PR-1a promoter-containing fragment is gel purified and cloned into pCGN1761ENX from which the double 35S promoter has been removed. This is done by cleavage with *XhoI* and blunting with T4

polymerase, followed by cleavage with *HindIII* and isolation of the larger vector-terminator containing fragment into which the pClB1004 promoter fragment is cloned. This generates a pCGN1761ENX derivative with the PR-1a promoter and the *tml* terminator and an intervening polylinker with unique *EcoRI* and *NotI* sites. The selected coding sequence can be inserted into this vector, and the fusion products (*i.e.* promoter-gene-terminator) can subsequently be transferred to any selected transformation vector, including those described *infra*. Various chemical regulators may be employed to induce expression of the selected coding sequence in the plants transformed according to the present invention, including the benzothiadiazole, isonicotinic acid, and salicylic acid compounds disclosed in U.S. Patent Nos. 5,523,311 and 5,614,395.

e. Inducible Expression, an Ethanol-Inducible Promoter:

A promoter inducible by certain alcohols or ketones, such as ethanol, may also be used to confer inducible expression of a coding sequence of the present invention. Such a promoter is for example the *alcA* gene promoter from *Aspergillus nidulans* (Caddick et al. (1998) *Nat. Biotechnol* 16:177-180). In *A. nidulans*, the *alcA* gene encodes alcohol dehydrogenase I, the expression of which is regulated by the AlcR transcription factors in presence of the chemical inducer. For the purposes of the present invention, the CAT coding sequences in plasmid p*alcA*:CAT comprising a *alcA* gene promoter sequence fused to a minimal 35S promoter (Caddick et al. (1998) *Nat. Biotechnol* 16:177-180) are replaced by a coding sequence of the present invention to form an expression cassette having the coding sequence under the control of the *alcA* gene promoter. This is carried out using methods well known in the art.

f. Inducible Expression, a Glucocorticoid-Inducible Promoter:

Induction of expression of a nucleic acid sequence of the present invention using systems based on steroid hormones is also contemplated. For example, a glucocorticoid-mediated induction system is used (Aoyama and Chua (1997) *The Plant Journal* 11: 605-612) and gene expression is induced by application of a glucocorticoid, for example a synthetic glucocorticoid, preferably dexamethasone, preferably at a concentration ranging from 0.1mM to 1mM, more preferably from 10mM to 100mM. For the purposes of the present invention, the luciferase gene sequences are replaced by a nucleic acid sequence of the invention to form an expression cassette having a nucleic acid sequence of the

invention under the control of six copies of the GAL4 upstream activating sequences fused to the 35S minimal promoter. This is carried out using methods well known in the art. The trans-acting factor comprises the GAL4 DNA-binding domain (Keegan et al. (1986) *Science* 231: 699-704) fused to the transactivating domain of the herpes viral protein VP16 (Triezenberg et al. (1988) *Genes Devel.* 2: 718-729) fused to the hormone-binding domain of the rat glucocorticoid receptor (Picard et al. (1988) *Cell* 54: 1073-1080). The expression of the fusion protein is controlled by any promoter suitable for expression in plants known in the art or described here. This expression cassette is also comprised in the plant comprising a nucleic acid sequence of the invention fused to the 6xGAL4/minimal promoter. Thus, tissue- or organ-specificity of the fusion protein is achieved leading to inducible tissue- or organ-specificity of the insecticidal toxin.

g. Root Specific Expression:

Another pattern of gene expression is root expression. A suitable root promoter is described by de Framond (FEBS 290: 103-106 (1991)) and also in the published patent application EP 0 452 269, which is herein incorporated by reference. This promoter is transferred to a suitable vector such as pCGN1761ENX for the insertion of a selected gene and subsequent transfer of the entire promoter-gene-terminator cassette to a transformation vector of interest.

h. Wound-Inducible Promoters:

Wound-inducible promoters may also be suitable for gene expression. Numerous such promoters have been described (e.g. Xu et al. *Plant Molec. Biol.* 22: 573-588 (1993), Logemann et al. *Plant Cell* 1: 151-158 (1989), Rohrmeier & Lehle, *Plant Molec. Biol.* 22: 783-792 (1993), Firek et al. *Plant Molec. Biol.* 22: 129-142 (1993), Warner et al. *Plant J.* 3: 191-201 (1993)) and all are suitable for use with the instant invention. Logemann et al. describe the 5' upstream sequences of the dicotyledonous potato *wun1* gene. Xu et al. show that a wound-inducible promoter from the dicotyledon potato (*pin2*) is active in the monocotyledon rice. Further, Rohrmeier & Lehle describe the cloning of the maize *Wip1* cDNA which is wound induced and which can be used to isolate the cognate promoter using standard techniques. Similar, Firek et al. and Warner et al. have described a wound-induced gene from the monocotyledon *Asparagus officinalis*, which is expressed at local wound and pathogen invasion sites. Using cloning techniques well known in the art, these

promoters can be transferred to suitable vectors, fused to the genes pertaining to this invention, and used to express these genes at the sites of plant wounding.

i. Pith-Preferred Expression:

Patent Application WO 93/07278, which is herein incorporated by reference, describes the isolation of the maize *trpA* gene, which is preferentially expressed in pith cells. The gene sequence and promoter extending up to -1726 bp from the start of transcription are presented. Using standard molecular biological techniques, this promoter, or parts thereof, can be transferred to a vector such as pCGN1761 where it can replace the 35S promoter and be used to drive the expression of a foreign gene in a pith-preferred manner. In fact, fragments containing the pith-preferred promoter or parts thereof can be transferred to any vector and modified for utility in transgenic plants.

j. Leaf-Specific Expression:

A maize gene encoding phosphoenol carboxylase (PEPC) has been described by Hudspeth & Grula (Plant Molec Biol 12: 579-589 (1989)). Using standard molecular biological techniques the promoter for this gene can be used to drive the expression of any gene in a leaf-specific manner in transgenic plants.

k. Pollen-Specific Expression:

WO 93/07278 describes the isolation of the maize calcium-dependent protein kinase (CDPK) gene which is expressed in pollen cells. The gene sequence and promoter extend up to 1400 bp from the start of transcription. Using standard molecular biological techniques, this promoter or parts thereof, can be transferred to a vector such as pCGN1761 where it can replace the 35S promoter and be used to drive the expression of a nucleic acid sequence of the invention in a pollen-specific manner.

2. Transcriptional Terminators

A variety of transcriptional terminators are available for use in expression cassettes. These are responsible for the termination of transcription beyond the transgene and its correct polyadenylation. Appropriate transcriptional terminators are those that are known to function in plants and include the CaMV 35S terminator, the *tm1* terminator, the nopaline synthase terminator and the pea *rbcS* E9 terminator. These can be used in both

monocotyledons and dicotyledons. In addition, a gene's native transcription terminator may be used.

3. Sequences for the Enhancement or Regulation of Expression

Numerous sequences have been found to enhance gene expression from within the transcriptional unit and these sequences can be used in conjunction with the genes of this invention to increase their expression in transgenic plants.

Various intron sequences have been shown to enhance expression, particularly in monocotyledonous cells. For example, the introns of the maize *Adh1* gene have been found to significantly enhance the expression of the wild-type gene under its cognate promoter when introduced into maize cells. Intron 1 was found to be particularly effective and enhanced expression in fusion constructs with the chloramphenicol acetyltransferase gene (Callis *et al.*, *Genes Develop.* 1: 1183-1200 (1987)). In the same experimental system, the intron from the maize *bronze1* gene had a similar effect in enhancing expression. Intron sequences have been routinely incorporated into plant transformation vectors, typically within the non-translated leader.

A number of non-translated leader sequences derived from viruses are also known to enhance expression, and these are particularly effective in dicotyledonous cells. Specifically, leader sequences from Tobacco Mosaic Virus (TMV, the "W-sequence"), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (*e.g.* Gallie *et al.* *Nucl. Acids Res.* 15: 8693-8711 (1987); Skuzeski *et al.* *Plant Molec. Biol.* 15: 65-79 (1990)).

4. Targeting of the Gene Product Within the Cell

Various mechanisms for targeting gene products are known to exist in plants and the sequences controlling the functioning of these mechanisms have been characterized in some detail. For example, the targeting of gene products to the chloroplast is controlled by a signal sequence found at the amino terminal end of various proteins which is cleaved during chloroplast import to yield the mature protein (*e.g.* Comai *et al.* *J. Biol. Chem.* 263: 15104-15109 (1988)). These signal sequences can be fused to heterologous gene products to effect the import of heterologous products into the chloroplast (van den Broeck, *et al.* *Nature* 313: 358-363 (1985)). DNA encoding for appropriate signal sequences can be isolated from the 5' end of the cDNAs encoding the RUBISCO protein, the CAB protein, the

EPSP synthase enzyme, the GS2 protein and many other proteins which are known to be chloroplast localized. *See also*, the section entitled "Expression With Chloroplast Targeting" in Example 37 of U.S. Patent No. 5,639,949.

Other gene products are localized to other organelles such as the mitochondrion and the peroxisome (*e.g.* Unger *et al.* Plant Molec. Biol. 13: 411-418 (1989)). The cDNAs encoding these products can also be manipulated to effect the targeting of heterologous gene products to these organelles. Examples of such sequences are the nuclear-encoded ATPases and specific aspartate amino transferase isoforms for mitochondria. Targeting cellular protein bodies has been described by Rogers *et al.* (Proc. Natl. Acad. Sci. USA 82: 6512-6516 (1985)).

In addition, sequences have been characterized which cause the targeting of gene products to other cell compartments. Amino terminal sequences are responsible for targeting to the ER, the apoplast, and extracellular secretion from aleurone cells (Koehler & Ho, Plant Cell 2: 769-783 (1990)). Additionally, amino terminal sequences in conjunction with carboxy terminal sequences are responsible for vacuolar targeting of gene products (Shinshi *et al.* Plant Molec. Biol. 14: 357-368 (1990)).

By the fusion of the appropriate targeting sequences described above to transgene sequences of interest it is possible to direct the transgene product to any organelle or cell compartment. For chloroplast targeting, for example, the chloroplast signal sequence from the RUBISCO gene, the CAB gene, the EPSP synthase gene, or the GS2 gene is fused in frame to the amino terminal ATG of the transgene. The signal sequence selected should include the known cleavage site, and the fusion constructed should take into account any amino acids after the cleavage site which are required for cleavage. In some cases this requirement may be fulfilled by the addition of a small number of amino acids between the cleavage site and the transgene ATG or, alternatively, replacement of some amino acids within the transgene sequence. Fusions constructed for chloroplast import can be tested for efficacy of chloroplast uptake by *in vitro* translation of *in vitro* transcribed constructions followed by *in vitro* chloroplast uptake using techniques described by Bartlett *et al.* In: Edelman *et al.* (Eds.) Methods in Chloroplast Molecular Biology, Elsevier pp 1081-1091 (1982) and Wasmann *et al.* Mol. Gen. Genet. 205: 446-453 (1986). These construction techniques are well known in the art and are equally applicable to mitochondria and peroxisomes.

The above-described mechanisms for cellular targeting can be utilized not only in conjunction with their cognate promoters, but also in conjunction with heterologous promoters so as to effect a specific cell-targeting goal under the transcriptional regulation of a promoter that has an expression pattern different to that of the promoter from which the targeting signal derives.

Example 24: Construction of Plant Transformation Vectors

Numerous transformation vectors available for plant transformation are known to those of ordinary skill in the plant transformation arts, and the genes pertinent to this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation. For certain target species, different antibiotic or herbicide selection markers may be preferred. Selection markers used routinely in transformation include the *nptII* gene, which confers resistance to kanamycin and related antibiotics (Messing & Vierra. Gene 19: 259-268 (1982); Bevan et al., Nature 304:184-187 (1983)), the *bar* gene, which confers resistance to the herbicide phosphinothricin (White et al., Nucl. Acids Res 18: 1062 (1990), Spencer et al. Theor. Appl. Genet 79: 625-631 (1990)), the *hph* gene, which confers resistance to the antibiotic hygromycin (Blochinger & Diggelmann, Mol Cell Biol 4: 2929-2931), and the *dhfr* gene, which confers resistance to methotrexate (Bourouis et al., EMBO J. 2(7): 1099-1104 (1983)), and the EPSPS gene, which confers resistance to glyphosate (U.S. Patent Nos. 4,940,935 and 5,188,642).

1. Vectors Suitable for *Agrobacterium* Transformation

Many vectors are available for transformation using *Agrobacterium tumefaciens*. These typically carry at least one T-DNA border sequence and include vectors such as pBIN19 (Bevan, Nucl. Acids Res. (1984)) and pXYZ. Below, the construction of two typical vectors suitable for *Agrobacterium* transformation is described.

a. pCIB200 and pCIB2001:

The binary vectors pCIB200 and pCIB2001 are used for the construction of recombinant vectors for use with *Agrobacterium* and are constructed in the following manner. pTJS75kan is created by *NarI* digestion of pTJS75 (Schmidhauser & Helinski, J.

Bacteriol. 164: 446-455 (1985)) allowing excision of the tetracycline-resistance gene, followed by insertion of an *AccI* fragment from pUC4K carrying an NPTII (Messing & Vierra, Gene 19: 259-268 (1982); Bevan et al., Nature 304: 184-187 (1983); McBride et al., Plant Molecular Biology 14: 266-276 (1990)). *XhoI* linkers are ligated to the *EcoRV* fragment of pCIB7 which contains the left and right T-DNA borders, a plant selectable *nos/nptII* chimeric gene and the pUC polylinker (Rothstein et al., Gene 53: 153-161 (1987)), and the *XhoI*-digested fragment are cloned into *Sall*-digested pTJS75kan to create pCIB200 (see also EP 0 332 104, example 19). pCIB200 contains the following unique polylinker restriction sites: *EcoRI*, *SstI*, *KpnI*, *BglII*, *XbaI*, and *Sall*. pCIB2001 is a derivative of pCIB200 created by the insertion into the polylinker of additional restriction sites. Unique restriction sites in the polylinker of pCIB2001 are *EcoRI*, *SstI*, *KpnI*, *BglII*, *XbaI*, *Sall*, *MluI*, *BclI*, *AvrII*, *ApaI*, *HpaI*, and *StuI*. pCIB2001, in addition to containing these unique restriction sites also has plant and bacterial kanamycin selection, left and right T-DNA borders for *Agrobacterium*-mediated transformation, the RK2-derived *trfA* function for mobilization between *E. coli* and other hosts, and the *OriT* and *OriV* functions also from RK2. The pCIB2001 polylinker is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

b. pCIB10 and Hygromycin Selection Derivatives thereof:

The binary vector pCIB10 contains a gene encoding kanamycin resistance for selection in plants and T-DNA right and left border sequences and incorporates sequences from the wide host-range plasmid pRK252 allowing it to replicate in both *E. coli* and *Agrobacterium*. Its construction is described by Rothstein et al. (Gene 53: 153-161 (1987)). Various derivatives of pCIB10 are constructed which incorporate the gene for hygromycin B phosphotransferase described by Gritz et al. (Gene 25: 179-188 (1983)). These derivatives enable selection of transgenic plant cells on hygromycin only (pCIB743), or hygromycin and kanamycin (pCIB715, pCIB717).

2. Vectors Suitable for non-*Agrobacterium* Transformation

Transformation without the use of *Agrobacterium tumefaciens* circumvents the requirement for T-DNA sequences in the chosen transformation vector and consequently vectors lacking these sequences can be utilized in addition to vectors such as the ones described above which contain T-DNA sequences. Transformation techniques that do not rely on *Agrobacterium* include transformation via particle bombardment, protoplast uptake

(e.g. PEG and electroporation) and microinjection. The choice of vector depends largely on the preferred selection for the species being transformed. Below, the construction of typical vectors suitable for non-*Agrobacterium* transformation is described.

a. pCIB3064:

pCIB3064 is a pUC-derived vector suitable for direct gene transfer techniques in combination with selection by the herbicide basta (or phosphinothricin). The plasmid pCIB246 comprises the CaMV 35S promoter in operational fusion to the *E. coli* GUS gene and the CaMV 35S transcriptional terminator and is described in the PCT published application WO 93/07278. The 35S promoter of this vector contains two ATG sequences 5' of the start site. These sites are mutated using standard PCR techniques in such a way as to remove the ATGs and generate the restriction sites *SspI* and *PvuII*. The new restriction sites are 96 and 37 bp away from the unique *Sall* site and 101 and 42 bp away from the actual start site. The resultant derivative of pCIB246 is designated pCIB3025. The GUS gene is then excised from pCIB3025 by digestion with *Sall* and *SacI*, the termini rendered blunt and religated to generate plasmid pCIB3060. The plasmid pJIT82 is obtained from the John Innes Centre, Norwich and the a 400 bp *SmaI* fragment containing the *bar* gene from *Streptomyces viridochromogenes* is excised and inserted into the *HpaI* site of pCIB3060 (Thompson *et al.* EMBO J 6: 2519-2523 (1987)). This generated pCIB3064, which comprises the *bar* gene under the control of the CaMV 35S promoter and terminator for herbicide selection, a gene for ampicillin resistance (for selection in *E. coli*) and a polylinker with the unique sites *SphI*, *PstI*, *HindIII*, and *BamHI*. This vector is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

b. pSOG19 and pSOG35:

pSOG35 is a transformation vector that utilizes the *E. coli* gene dihydrofolate reductase (DFR) as a selectable marker conferring resistance to methotrexate. PCR is used to amplify the 35S promoter (-800 bp), intron 6 from the maize *Adh1* gene (-550 bp) and 18 bp of the GUS untranslated leader sequence from pSOG10. A 250-bp fragment encoding the *E. coli* dihydrofolate reductase type II gene is also amplified by PCR and these two PCR fragments are assembled with a *SacI*-*PstI* fragment from pB1221 (Clontech) which comprises the pUC19 vector backbone and the nopaline synthase terminator. Assembly of these fragments generates pSOG19 which contains the 35S promoter in fusion

with the intron 6 sequence, the GUS leader, the DHFR gene and the nopaline synthase terminator. Replacement of the GUS leader in pSOG19 with the leader sequence from Maize Chlorotic Mottle Virus (MCMV) generates the vector pSOG35. pSOG19 and pSOG35 carry the pUC gene for ampicillin resistance and have *HindIII*, *SphI*, *PstI* and *EcoRI* sites available for the cloning of foreign substances.

Example 25: Transformation

Once a nucleic acid sequence of the invention has been cloned into an expression system, it is transformed into a plant cell. Methods for transformation and regeneration of plants are well known in the art. For example, Ti plasmid vectors have been utilized for the delivery of foreign DNA, as well as direct DNA uptake, liposomes, electroporation, microinjection, and microprojectiles. In addition, bacteria from the genus *Agrobacterium* can be utilized to transform plant cells. Below are descriptions of representative techniques for transforming both dicotyledonous and monocotyledonous plants.

1. Transformation of Dicotyledons

Transformation techniques for dicotyledons are well known in the art and include *Agrobacterium*-based techniques and techniques that do not require *Agrobacterium*. Non-*Agrobacterium* techniques involve the uptake of exogenous genetic material directly by protoplasts or cells. This can be accomplished by PEG or electroporation mediated uptake, particle bombardment-mediated delivery, or microinjection. Examples of these techniques are described by Paszkowski *et al.*, EMBO J 3: 2717-2722 (1984), Potrykus *et al.*, Mol. Gen. Genet. 199: 169-177 (1985), Reich *et al.*, Biotechnology 4: 1001-1004 (1986), and Klein *et al.*, Nature 327: 70-73 (1987). In each case the transformed cells are regenerated to whole plants using standard techniques known in the art.

Agrobacterium-mediated transformation is a preferred technique for transformation of dicotyledons because of its high efficiency of transformation and its broad utility with many different species. *Agrobacterium* transformation typically involves the transfer of the binary vector carrying the foreign DNA of interest (e.g. pCIB200 or pCIB2001) to an appropriate *Agrobacterium* strain which may depend of the complement of *vir* genes carried by the host *Agrobacterium* strain either on a co-resident Ti plasmid or chromosomally (e.g. strain CIB542 for pCIB200 and pCIB2001 (Uknes *et al.* Plant Cell 5: 159-169 (1993)). The

transfer of the recombinant binary vector to *Agrobacterium* is accomplished by a triparental mating procedure using *E. coli* carrying the recombinant binary vector, a helper *E. coli* strain which carries a plasmid such as pRK2013 and which is able to mobilize the recombinant binary vector to the target *Agrobacterium* strain. Alternatively, the recombinant binary vector can be transferred to *Agrobacterium* by DNA transformation (Höfgen & Willmitzer, Nucl. Acids Res. 16: 9877 (1988)).

Transformation of the target plant species by recombinant *Agrobacterium* usually involves co-cultivation of the *Agrobacterium* with explants from the plant and follows protocols well known in the art. Transformed tissue is regenerated on selectable medium carrying the antibiotic or herbicide resistance marker present between the binary plasmid T-DNA borders.

Another approach to transforming plant cells with a gene involves propelling inert or biologically active particles at plant tissues and cells. This technique is disclosed in U.S. Patent Nos. 4,945,050, 5,036,006, and 5,100,792 all to Sanford et al. Generally, this procedure involves propelling inert or biologically active particles at the cells under conditions effective to penetrate the outer surface of the cell and afford incorporation within the interior thereof. When inert particles are utilized, the vector can be introduced into the cell by coating the particles with the vector containing the desired gene. Alternatively, the target cell can be surrounded by the vector so that the vector is carried into the cell by the wake of the particle. Biologically active particles (e.g., dried yeast cells, dried bacterium or a bacteriophage, each containing DNA sought to be introduced) can also be propelled into plant cell tissue.

2. Transformation of Monocotyledons

Transformation of most monocotyledon species has now also become routine. Preferred techniques include direct gene transfer into protoplasts using PEG or electroporation techniques, and particle bombardment into callus tissue. Transformations can be undertaken with a single DNA species or multiple DNA species (*i.e.* co-transformation) and both these techniques are suitable for use with this invention. Co-transformation may have the advantage of avoiding complete vector construction and of generating transgenic plants with unlinked loci for the gene of interest and the selectable marker, enabling the removal of the selectable marker in subsequent generations, should this be regarded desirable. However, a disadvantage of the use of co-transformation is the

less than 100% frequency with which separate DNA species are integrated into the genome (Schocher *et al.* *Biotechnology* 4: 1093-1096 (1986)).

Patent Applications EP 0 292 435, EP 0 392 225, and WO 93/07278 describe techniques for the preparation of callus and protoplasts from an elite inbred line of maize, transformation of protoplasts using PEG or electroporation, and the regeneration of maize plants from transformed protoplasts. Gordon-Kamm *et al.* (*Plant Cell* 2: 603-618 (1990)) and Fromm *et al.* (*Biotechnology* 8: 833-839 (1990)) have published techniques for transformation of A188-derived maize line using particle bombardment. Furthermore, WO 93/07278 and Koziel *et al.* (*Biotechnology* 11: 194-200 (1993)) describe techniques for the transformation of elite inbred lines of maize by particle bombardment. This technique utilizes immature maize embryos of 1.5-2.5 mm length excised from a maize ear 14-15 days after pollination and a PDS-1000He Biolistics device for bombardment.

Transformation of rice can also be undertaken by direct gene transfer techniques utilizing protoplasts or particle bombardment. Protoplast-mediated transformation has been described for *Japonica*-types and *Indica*-types (Zhang *et al.* *Plant Cell Rep* 7: 379-384 (1988); Shimamoto *et al.* *Nature* 338: 274-277 (1989); Datta *et al.* *Biotechnology* 8: 736-740 (1990)). Both types are also routinely transformable using particle bombardment (Christou *et al.* *Biotechnology* 9: 957-962 (1991)). Furthermore, WO 93/21335 describes techniques for the transformation of rice via electroporation.

Patent Application EP 0 332 581 describes techniques for the generation, transformation and regeneration of Pooidae protoplasts. These techniques allow the transformation of *Dactylis* and wheat. Furthermore, wheat transformation has been described by Vasil *et al.* (*Biotechnology* 10: 667-674 (1992)) using particle bombardment into cells of type C long-term regenerable callus, and also by Vasil *et al.* (*Biotechnology* 11: 1553-1558 (1993)) and Weeks *et al.* (*Plant Physiol.* 102: 1077-1084 (1993)) using particle bombardment of immature embryos and immature embryo-derived callus. A preferred technique for wheat transformation, however, involves the transformation of wheat by particle bombardment of immature embryos and includes either a high sucrose or a high maltose step prior to gene delivery. Prior to bombardment, any number of embryos (0.75-1 mm in length) are plated onto MS medium with 3% sucrose (Murashiga & Skoog, *Physiologia Plantarum* 15: 473-497 (1962)) and 3 mg/l 2,4-D for induction of somatic embryos, which is allowed to proceed in the dark. On the chosen day of bombardment, embryos are removed from the induction medium and placed onto the osmoticum (*i.e.*

induction medium with sucrose or maltose added at the desired concentration, typically 15%). The embryos are allowed to plasmolyze for 2-3 h and are then bombarded. Twenty embryos per target plate is typical, although not critical. An appropriate gene-carrying plasmid (such as pCIB3064 or pSG35) is precipitated onto micrometer size gold particles using standard procedures. Each plate of embryos is shot with the DuPont Biolistics® helium device using a burst pressure of ~1000 psi using a standard 80 mesh screen. After bombardment, the embryos are placed back into the dark to recover for about 24 h (still on osmoticum). After 24 hrs, the embryos are removed from the osmoticum and placed back onto induction medium where they stay for about a month before regeneration. Approximately one month later the embryo explants with developing embryogenic callus are transferred to regeneration medium (MS + 1 mg/liter NAA, 5 mg/liter GA), further containing the appropriate selection agent (10 mg/l basta in the case of pCIB3064 and 2 mg/l methotrexate in the case of pSOG35). After approximately one month, developed shoots are transferred to larger sterile containers known as "GA7s" which contain half-strength MS, 2% sucrose, and the same concentration of selection agent.

Transformation of monocotyledons using *Agrobacterium* has also been described. See, WO 94/00977 and U.S. Patent No. 5,591,616, both of which are incorporated herein by reference.

E. Breeding and Seed Production

Example 26: Breeding

The plants obtained via transformation with a nucleic acid sequence of the present invention can be any of a wide variety of plant species, including those of monocots and dicots; however, the plants used in the method of the invention are preferably selected from the list of agronomically important target crops set forth *supra*. The expression of a gene of the present invention in combination with other characteristics important for production and quality can be incorporated into plant lines through breeding. Breeding approaches and techniques are known in the art. See, for example, Welsh J. R., *Fundamentals of Plant Genetics and Breeding*, John Wiley & Sons, NY (1981); *Crop Breeding*, Wood D. R. (Ed.) American Society of Agronomy Madison, Wisconsin (1983); Mayo O., *The Theory of Plant Breeding*, Second Edition, Clarendon Press, Oxford (1987); Singh, D.P., *Breeding for*

Resistance to Diseases and Insect Pests, Springer-Verlag, NY (1986); and Wricke and Weber, *Quantitative Genetics and Selection Plant Breeding*, Walter de Gruyter and Co., Berlin (1986).

The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction or vegetative growth and can thus be maintained and propagated in progeny plants. Generally said maintenance and propagation make use of known agricultural methods developed to fit specific purposes such as tilling, sowing or harvesting. Specialized processes such as hydroponics or greenhouse technologies can also be applied. As the growing crop is vulnerable to attack and damages caused by insects or infections as well as to competition by weed plants, measures are undertaken to control weeds, plant diseases, insects, nematodes, and other adverse conditions to improve yield. These include mechanical measures such a tillage of the soil or removal of weeds and infected plants, as well as the application of agrochemicals such as herbicides, fungicides, gametocides, nematocides, growth regulants, ripening agents and insecticides.

Use of the advantageous genetic properties of the transgenic plants and seeds according to the invention can further be made in plant breeding, which aims at the development of plants with improved properties such as tolerance of pests, herbicides, or stress, improved nutritional value, increased yield, or improved structure causing less loss from lodging or shattering. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate progeny plants. Depending on the desired properties, different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical, or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines, that for example, increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow one to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained, which, due to their optimized genetic "equipment", yield harvested product of

better quality than products that were not able to tolerate comparable adverse developmental conditions.

Example 27: Seed Production

In seed production, germination quality and uniformity of seeds are essential product characteristics, whereas germination quality and uniformity of seeds harvested and sold by the farmer is not important. As it is difficult to keep a crop free from other crop and weed seeds, to control seedborne diseases, and to produce seed with good germination, fairly extensive and well-defined seed production practices have been developed by seed producers, who are experienced in the art of growing, conditioning and marketing of pure seed. Thus, it is common practice for the farmer to buy certified seed meeting specific quality standards instead of using seed harvested from his own crop. Propagation material to be used as seeds is customarily treated with a protectant coating comprising herbicides, insecticides, fungicides, bactericides, nematocides, molluscicides, or mixtures thereof. Customarily used protectant coatings comprise compounds such as captan, carboxin, thiram (TMTD®), methalaxyl (Apron®), and pirimiphos-methyl (Actellic®). If desired, these compounds are formulated together with further carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation to provide protection against damage caused by bacterial, fungal or animal pests. The protectant coatings may be applied by impregnating propagation material with a liquid formulation or by coating with a combined wet or dry formulation. Other methods of application are also possible such as treatment directed at the buds or the fruit.

It is a further aspect of the present invention to provide new agricultural methods, such as the methods exemplified above, which are characterized by the use of transgenic plants, transgenic plant material, or transgenic seed according to the present invention.

The seeds may be provided in a bag, container or vessel comprised of a suitable packaging material, the bag or container capable of being closed to contain seeds. The bag, container or vessel may be designed for either short term or long term storage, or both, of the seed. Examples of a suitable packaging material include paper, such as kraft paper, rigid or pliable plastic or other polymeric material, glass or metal. Desirably the bag, container, or vessel is comprised of a plurality of layers of packaging materials, of the same or differing type. In one embodiment the bag, container or vessel is provided so as to

exclude or limit water and moisture from contacting the seed. In one example, the bag, container or vessel is sealed, for example heat sealed, to prevent water or moisture from entering. In another embodiment water absorbent materials are placed between or adjacent to packaging material layers. In yet another embodiment the bag, container or vessel, or packaging material of which it is comprised is treated to limit, suppress or prevent disease, contamination or other adverse affects of storage or transport of the seed. An example of such treatment is sterilization, for example by chemical means or by exposure to radiation. Comprised by the present invention is a commercial bag comprising seed of a transgenic plant comprising a gene of the present invention that is expressed in said transformed plant at higher levels than in a wild type plant, together with a suitable carrier, together with label instructions for the use thereof for conferring broad spectrum disease resistance to plants.

**BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT
OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURES**

INTERNATIONAL FORM

TO

Novartis AG
Novartis Corporation
3054 Cornwallis Rd.
Research Triangle Park,
NC 27709

VIABILITY STATEMENT

Issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

NAME AND ADDRESS OF THE PARTY TO WHOM
THE VIABILITY STATEMENT IS ISSUED

I. DEPOSITOR Name: Novartis AG Novartis Corporation Address: 3054 Cornwallis Rd. Research Triangle Park, NC 27709	II. IDENTIFICATION OF THE MICROORGANISM Depositor's taxonomic designation and accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: <i>Escherichia coli</i> NRRL B-30077 Date of: October 28, 1998 <input checked="" type="checkbox"/> Original Deposit <input type="checkbox"/> New Deposit <input type="checkbox"/> Repropagation of Original Deposit		
III. (a) VIABILITY STATEMENT Deposit was found: <input checked="" type="checkbox"/> Viable <input type="checkbox"/> Nonviable on October 31, 1998 (Date) International Depositary Authority's preparation was found viable on December 8, 1998 (Date) ¹			
III. (b) DEPOSITOR'S EQUIVALENCY DECLARATION Depositor determined the International Depositary Authority's preparation was <input checked="" type="checkbox"/> Equivalent <input type="checkbox"/> Not equivalent to deposit on <u>1-6-99</u> (Date) Signature of Depositor <u>Hope Hunt</u>			
IV. CONDITIONS UNDER WHICH THE VIABILITY TEST WAS PERFORMED (Depositor/Depository)¹ The dried culture was put into 2mls LBampicillin and grown at 37°C overnight with shaking. Some of the liquid culture was streaked to an LBampicillin plate + grown at 37°C overnight.			
V. INTERNATIONAL DEPOSITARY AUTHORITY <table border="1"> <tr> <td data-bbox="183 1499 737 1656"> Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A. </td> <td data-bbox="737 1499 1344 1656"> Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): <u>P. J. [Signature]</u> Date: 12-3-98 </td> </tr> </table>		Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): <u>P. J. [Signature]</u> Date: 12-3-98
Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): <u>P. J. [Signature]</u> Date: 12-3-98		

¹ Indicate the date of the original deposit or when a new deposit has been made.

² Mark with a cross the applicable box.

³ In the cases referred to in Rule 10.2(a)(ii) and (iii), refer to the most recent viability test.

⁴ Fill in if the information has been requested.

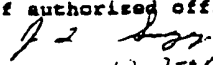
**BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSE OF PATENT PROCEDURES**

INTERNATIONAL FORM

TO
Novartis AG
Novartis Corporation
3054 Cornwallis Rd.
Research Triangle Park,
NC 27709

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

**NAME AND ADDRESS
OF DEPOSITOR**

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: <i>Escherichia coli</i> pNOV2400	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: NRRL B-30077
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
The microorganism identified under I. above was accompanied by:	
<input type="checkbox"/> a scientific description <input checked="" type="checkbox"/> a proposed taxonomic designation (Mark with a cross where applicable)	
III. RECEIPT AND ACCEPTANCE	
This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on October 28, 1998 (date of the original deposit) ¹	
IV. RECEIPT OF REQUEST FOR CONVERSION	
The microorganism identified under I. above was received by this International Depositary Authority on _____ (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on _____ (date of receipt of request for conversion).	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):  Date: 12-3-98

¹ Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.

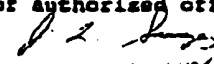
**BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSE OF PATENT PROCEDURES**

INTERNATIONAL FORM

TO
Novartis AG
Novartis Corporation
3054 Cornwallis Rd.
Research Triangle Park,
NC 27709

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

**NAME AND ADDRESS
OF DEPOSITOR**

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: <i>Escherichia coli</i> pNOV1001	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: NRRL B-30078
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
The microorganism identified under I. above was accompanied by:	
<input type="checkbox"/> a scientific description <input checked="" type="checkbox"/> a proposed taxonomic designation (Mark with a cross where applicable)	
III. RECEIPT AND ACCEPTANCE	
This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on October 28, 1998 (date of the original deposit) ¹	
IV. RECEIPT OF REQUEST FOR CONVERSION	
The microorganism identified under I. above was received by this International Depositary Authority on _____ (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on _____ (date of receipt of request for conversion).	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):  Date: 12-3-98

¹ Where Rule 6.4(d) applies, such data is the date on which the status of international depositary authority was acquired.

**BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT
OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURES**

INTERNATIONAL FORM

TO

Novartis AG
Novartis Corporation
3054 Cornwallis Rd.
Research Triangle Park,
NC 27709

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

NAME AND ADDRESS OF THE PARTY TO WHOM
THE VIABILITY STATEMENT IS ISSUED

I. DEPOSITOR Name: Novartis AG Novartis Corporation Address: 3054 Cornwallis Rd. Research Triangle Park, NC 27709	II. IDENTIFICATION OF THE MICROORGANISM Depositor's taxonomic designation and accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: <i>Escherichia coli</i> NRRL B-30078 Date of: October 28, 1998 <input checked="" type="checkbox"/> ¹ Original Deposit <input type="checkbox"/> ² New Deposit <input type="checkbox"/> ³ Repropagation of Original Deposit		
III. (a) VIABILITY STATEMENT Deposit was found: <input checked="" type="checkbox"/> Viable <input type="checkbox"/> Nonviable on October 31, 1998 (Date) International Depositary Authority's preparation was found viable on December 8, 1998 (Date) ³			
III. (b) DEPOSITOR'S EQUIVALENCY DECLARATION Depositor determined the International Depositary Authority's preparation was <input checked="" type="checkbox"/> ¹ Equivalent <input type="checkbox"/> ² Not equivalent to deposit on <u>1-6-99</u> (Date) Signature of Depositor <u>Hope Hart</u>			
IV. CONDITIONS UNDER WHICH THE VIABILITY TEST WAS PERFORMED (Depositor/Depository)¹ <u>The dried culture was put into 2mLs LBamp(100µg/mL) and grown at 37°C overnight with shaking. Some of the liquid culture was streaked to an LBamp plate and grown at 37°C overnight.</u>			
V. INTERNATIONAL DEPOSITARY AUTHORITY <table border="0"> <tr> <td data-bbox="203 1438 771 1638"> Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A. </td> <td data-bbox="771 1438 1362 1638"> Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): <u>[Signature]</u> Date: <u>12-3-98</u> </td> </tr> </table>		Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): <u>[Signature]</u> Date: <u>12-3-98</u>
Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): <u>[Signature]</u> Date: <u>12-3-98</u>		

- ¹ Indicate the date of the original deposit or when a new deposit has been made.
² Mark with a cross the applicable box.
³ In the cases referred to in Rule 10.2(a)(ii) and (iii), refer to the most recent viability test.
⁴ Fill in if the information has been requested.

BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSE OF PATENT PROCEDURES

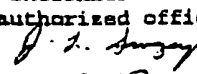
INTERNATIONAL FORM

TO

Novartis Corp.
c/o Novartis AG
P. O. Box 12257
Research Triangle Park, NC 27709

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

NAME AND ADDRESS
OF DEPOSITOR

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: Bacteria sp. pCIB 9359-7	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: NRRL B-21835
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
The microorganism identified under I. above was accompanied by:	
<input checked="" type="checkbox"/> a scientific description	
<input type="checkbox"/> a proposed taxonomic designation	
(Mark with a cross where applicable)	
III. RECEIPT AND ACCEPTANCE	
This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on September 17, 1997 (date of the original deposit) ¹	
IV. RECEIPT OF REQUEST FOR CONVERSION	
The microorganism identified under I. above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):  Date: 11-13-97

¹ Where Rule 6.4(d) applies, such date is the date on which the status of international
depositary authority was acquired.

**BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT
OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURES**

INTERNATIONAL FORM

TO

Novartis Corp.
c/o Novartis AG
P. O. Box 12257
Research Triangle Park, NC 27709

VIABILITY STATEMENT

issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

**NAME AND ADDRESS OF THE PARTY TO WHOM
THE VIABILITY STATEMENT IS ISSUED**

I. DEPOSITOR Name: Novartis Corp c/o Novartis AG Address: P. O. Box 12257 Research Triangle Park, NC 27709	II. IDENTIFICATION OF THE MICROORGANISM Depositor's taxonomic designation and accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: Bacteria sp. NRRL B-21835 Date of: September 17, 1997 <input checked="" type="checkbox"/> : Original Deposit <input type="checkbox"/> : New Deposit <input type="checkbox"/> : Repropagation of Original Deposit		
III. (a) VIABILITY STATEMENT Deposit was found: <input checked="" type="checkbox"/> Viable <input type="checkbox"/> Nonviable on September 18, 1997 (Date) International Depositary Authority's preparation was found viable on September 25, 1997 (Date) ¹			
III. (b) DEPOSITOR'S EQUIVALENCY DECLARATION Depositor determined the International Depositary Authority's preparation was <input type="checkbox"/> : Equivalent <input type="checkbox"/> : Not equivalent to deposit on _____ (Date) Signature of Depositor _____			
IV. CONDITIONS UNDER WHICH THE VIABILITY TEST WAS PERFORMED (Depositors/Depositary)¹ 			
V. INTERNATIONAL DEPOSITARY AUTHORITY <table border="0"> <tr> <td data-bbox="203 1491 769 1646"> Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A. </td> <td data-bbox="769 1491 1362 1646"> Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): <div style="text-align: center;"><i>J. Z. Long</i></div> Date: 11-17-97 </td> </tr> </table>		Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): <div style="text-align: center;"><i>J. Z. Long</i></div> Date: 11-17-97
Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): <div style="text-align: center;"><i>J. Z. Long</i></div> Date: 11-17-97		

¹ Indicate the date of the original deposit or when a new deposit had been made.
² Mark with a cross the applicable box.
³ In the cases referred to in Rule 10.2(a)(iii) and (iii), refer to the most recent viability test.
⁴ Fill in if the information has been requested.

What is claimed is:

1. An isolated nucleic acid molecule comprising:

- (a) a nucleotide sequence substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 15,171-18,035 of SEQ ID NO:11, and nucleotides 31,393-35,838 of SEQ ID NO:11;
- (b) a nucleotide sequence comprising nucleotides 23,768-31,336 of SEQ ID NO:11; or
- (c) a nucleotide sequence isocoding with the nucleotide sequence of (a) or (b);

wherein expression of said nucleic acid molecule results in at least one toxin that is active against insects.

2. An isolated nucleic acid molecule comprising a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of a nucleotide sequence selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 15,171-18,035 of SEQ ID NO:11, and nucleotides 31,393-35,838 of SEQ ID NO:11, wherein expression of said nucleic acid molecule results in at least one toxin that is active against insects.

3. An isolated nucleic acid molecule comprising a nucleotide sequence from *Photobacterium luminescens* selected from the group consisting of: nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, nucleotides 4515-9269 of SEQ ID NO:1, nucleotides 66-1898 of SEQ ID NO:11, nucleotides 2416-9909 of SEQ ID NO:11, the complement of nucleotides 2817-3395 of SEQ ID NO:11, nucleotides 9966-14,633 of SEQ ID NO:11, nucleotides 14,699-15,007 of SEQ ID NO:11, nucleotides 15,171-18,035 of SEQ ID NO:11, the complement of nucleotides 17,072-17,398 of SEQ ID NO:11, the complement of nucleotides 18,235-19,167 of SEQ ID NO:11, the complement of nucleotides 19,385-20,116 of SEQ ID NO:11, the complement of nucleotides 20,217-20,963 of SEQ ID NO:11,

the complement of nucleotides 22,172-23,086 of SEQ ID NO:11, nucleotides 23,768-31,336 of SEQ ID NO:11, nucleotides 31,393-35,838 of SEQ ID NO:11, the complement of nucleotides 35,383-35,709 of SEQ ID NO:11, the complement of nucleotides 36,032-36,661 of SEQ ID NO:11, and the complement of nucleotides 36,654-37,781 of SEQ ID NO:11.

4. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence is substantially similar to nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

5. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence encodes an amino acid sequence selected from the group consisting of SEQ ID NOs:2-6.

6. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence comprises nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides 2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

7. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence is substantially similar to nucleotides 15,171-18,035 or 31,393-35,838 of SEQ ID NO:11.

8. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NOs:12-14.

9. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence comprises nucleotides 15,171-18,035; 23,768-31,336; or 31,393-35,838 of SEQ ID NO:11.

10. An isolated nucleic acid molecule according to claim 2, comprising a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 412-1665 of SEQ ID NO:1, nucleotides 1686-2447 of SEQ ID NO:1, nucleotides

2758-3318 of SEQ ID NO:1, nucleotides 3342-4118 of SEQ ID NO:1, or nucleotides 4515-9269 of SEQ ID NO:1.

11. An isolated nucleic acid molecule according to claim 2, comprising a 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair nucleotide portion of nucleotides 15,171-18,035 or 31,393-35,838 of SEQ ID NO:11.
 12. A chimeric gene comprising a heterologous promoter sequence operatively linked to the nucleic acid molecule of claim 1 or claim 2.
 13. A recombinant vector comprising the chimeric gene of claim 12.
 14. A host cell comprising the chimeric gene of claim 12.
 15. A host cell according to claim 14, which is a bacterial cell.
 16. A host cell according to claim 14, which is a yeast cell.
 17. A host cell according to claim 14, which is a plant cell.
 18. A plant comprising the plant cell of claim 17.
 19. A plant according to claim 18, which is maize.
 20. A toxin produced by the expression of a DNA molecule according to claim 1 or claim 2.
 21. A toxin according to claim 20, wherein said toxin has activity against Lepidopteran insects.
 22. A toxin according to claim 21, wherein said toxin has activity against *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm).
-

23. A toxin according to claim 20, wherein said toxin has activity against Lepidopteran and Coleopteran insects.

24. A toxin according to claim 23, wherein said toxin has insecticidal activity against *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

25. A toxin according to claim 20, wherein said toxin comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs:2-6.

26. A toxin according to claim 20, wherein said toxin comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs:12-14.

27. A composition comprising an insecticidally effective amount of a toxin according to claim 20.

28. A method of producing a toxin that is active against insects, comprising:

- (a) obtaining the host cell of claim 14; and
- (b) expressing the nucleic acid molecule in said cell, which results in at least one toxin that is active against insects.

29. A method of producing an insect-resistant plant, comprising introducing a nucleic acid molecule according to claim 1 into said plant, wherein said nucleic acid molecule is expressible in said plant in an effective amount to control insects.

30. A method of controlling insects comprising delivering to the insects an effective amount of a toxin according to claim 44.

31. The method of claim 29 or claim 30, wherein the insects are Lepidopteran insects.

32. The method of claim 31, wherein the insects are selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Trichoplusia ni* (Cabbage Looper), *Ostrinia nubilalis* (European Corn Borer), *Heliothis virescens* (Tobacco Budworm), *Helicoverpa zea* (Corn Earworm), *Spodoptera exigua* (Beet Armyworm), and *Spodoptera frugiperda* (Fall Armyworm).

33. The method of claim 29 or claim 30, wherein the insects are Lepidopteran and Coleopteran insects.

34. The method of claim 33, wherein the insects are selected from the group consisting of: *Plutella xylostella* (Diamondback Moth), *Ostrinia nubilalis* (European Corn Borer), and *Manduca sexta* (Tobacco Hornworm), *Diabrotica virgifera virgifera* (Western Corn Rootworm), *Diabrotica undecimpunctata howardi* (Southern Corn Rootworm), and *Leptinotarsa decimlineata* (Colorado Potato Beetle).

35. The method of claim 30, wherein the toxin is delivered to the insects orally.

36. A method for mutagenizing a nucleic acid molecule according to claim 1, wherein the nucleic acid molecule has been cleaved into population of double-stranded random fragments of a desired size, comprising:

- (a) adding to the population of double-stranded random fragments one or more single- or double-stranded oligonucleotides, wherein said oligonucleotides each comprise an area of identity and an area of heterology to a double-stranded template polynucleotide;
- (b) denaturing the resultant mixture of double-stranded random fragments and oligonucleotides into single-stranded fragments;
- (c) incubating the resultant population of single-stranded fragments with a polymerase under conditions which result in the annealing of said single-stranded fragments at said areas of identity to form pairs of annealed fragments, said areas of identity being sufficient for one member of a pair to prime replication of the other, thereby forming a mutagenized double-stranded polynucleotide; and

- (d) repeating the second and third steps for at least two further cycles, wherein the resultant mixture in the second step of a further cycle includes the mutagenized double-stranded polynucleotide from the third step of the previous cycle, and wherein the further cycle forms a further mutagenized double-stranded polynucleotide.
-

SEQUENCE LISTING

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5

10

15

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165 170 175	
gaa att att cgc tca ggg cgg gca aaa tgt atg att gcc gga gcc gct	993
Glu Ile Ile Arg Ser Gly Arg Ala Lys Cys Met Ile Ala Gly Ala Ala	
180 185 190	
gaa tca ctc acg cgg gaa tgt aat att tgg agt att gat gta ctg aat	1041
Glu Ser Leu Thr Arg Glu Cys Asn Ile Trp Ser Ile Asp Val Leu Asn	
195 200 205 210	
gca tta tcg aaa gaa caa gcg gac cca aat ctt gca tgt tgt cca ttt	1089
Ala Leu Ser Lys Glu Gln Ala Asp Pro Asn Leu Ala Cys Cys Pro Phe	
215 220 225	
agc ctt gat cgc tct gga ttt gta tta gcc gaa gga gcg gcg gta gtt	1137
Ser Leu Asp Arg Ser Gly Phe Val Leu Ala Glu Gly Ala Ala Val Val	
230 235 240	
tgt ctg gaa aat tat gat tca gcc atc gcg cgt ggt gca acg att tta	1185
Cys Leu Glu Asn Tyr Asp Ser Ala Ile Ala Arg Gly Ala Thr Ile Leu	
245 250 255	
gcg gaa att aaa ggt tac gcc caa tat tca gat gcc gtt aat tta acc	1233
Ala Glu Ile Lys Gly Tyr Ala Gln Tyr Ser Asp Ala Val Asn Leu Thr	
260 265 270	

cgg cca aca gaa gat att gaa cct aaa ata tta gcg ata act aaa gcc 1281
 Arg Pro Thr Glu Asp Ile Glu Pro Lys Ile Leu Ala Ile Thr Lys Ala
 275 280 285 290

att gag cag gca cag att tcg ccg aaa gat att gac tac att aat gct 1329
 Ile Glu Gln Ala Gln Ile Ser Pro Lys Asp Ile Asp Tyr Ile Asn Ala
 295 300 305

cat ggt act tct aca ccg tta aat gat ctt tat gaa act cag gca att 1377
 His Gly Thr Ser Thr Pro Leu Asn Asp Leu Tyr Glu Thr Gln Ala Ile
 310 315 320

aaa gca gca ctg ggc caa tat gct tat cag gta cct ata tca agc aca 1425
 Lys Ala Ala Leu Gly Gln Tyr Ala Tyr Gln Val Pro Ile Ser Ser Thr
 325 330 335

aaa tct tat acc ggc cac ctt att gct gcc gcc ggt agt ttt gaa acg 1473
 Lys Ser Tyr Thr Gly His Leu Ile Ala Ala Ala Gly Ser Phe Glu Thr
 340 345 350

att gta tgt gtg aaa gca tta gct gaa aat tgc ttg cca gca aca ttg 1521
 Ile Val Cys Val Lys Ala Leu Ala Glu Asn Cys Leu Pro Ala Thr Leu
 355 360 365 370

aat tta cac cgg gcc gat cca gat tgc gat ctc aat tat ttg cct aat 1569
 Asn Leu His Arg Ala Asp Pro Asp Cys Asp Leu Asn Tyr Leu Pro Asn
 375 380 385

caa cat tgc tac acc gct caa cca gag gtg aca ctc aat att agc gca 1617
 Gln His Cys Tyr Thr Ala Gln Pro Glu Val Thr Leu Asn Ile Ser Ala
 390 395 400

ggt ttc ggc ggg cat aac gct gcg ttg gtt atc gct aag gta agg taa 1665
 Gly Phe Gly Gly His Asn Ala Ala Leu Val Ile Ala Lys Val Arg
 405 410 415

ctgatatgtt gatttttgcg atg gaa gat att gaa cat tgg tcg aat ttc tct 1718
 Met Glu Asp Ile Glu His Trp Ser Asn Phe Ser
 420 425

ggg gat ttt aac ccc atc cat tat tcg gcg aaa agc gag tct ttg cgc 1766
 Gly Asp Phe Asn Pro Ile His Tyr Ser Ala Lys Ser Glu Ser Leu Arg
 430 435 440 445

aat ata cag caa cac ccg gtg cag gga atg ttg agt ttg ctc tat gta 1814
 Asn Ile Gln Gln His Pro Val Gln Gly Met Leu Ser Leu Leu Tyr Val
 450 455 460

cgg caa cag ttt tct caa tta act tcc gct ttt aca acg gga ata ttg 1862
 Arg Gln Gln Phe Ser Gln Leu Thr Ser Ala Phe Thr Thr Gly Ile Leu
 465 470 475

aac att gat gcc tct ttc cgc cag tat gtt tat acc gca tta ccc cat 1910
 Asn Ile Asp Ala Ser Phe Arg Gln Tyr Val Tyr Thr Ala Leu Pro His
 480 485 490

caa ctg agg att aat act aaa aac aaa acg ttt aaa tta gaa aat ccc 1958
 Gln Leu Arg Ile Asn Thr Lys Asn Lys Thr Phe Lys Leu Glu Asn Pro
 495 500 505

agt aaa gaa aac acg ttg ttc ggc aat acc agc gta gag aat aca atg 2006
 Ser Lys Glu Asn Thr Leu Phe Gly Asn Thr Ser Val Glu Asn Thr Met
 510 515 520 525

gag tca att gaa gat tgg atc gtt cag gat aat tgt caa aaa cta acg 2054

Glu Ser Ile Glu Asp Trp Ile Val Gln Asp Asn Cys Gln Lys Leu Thr	
530 535 540	
ata aca ggg gag gaa gtt tgt gaa aag tat gct gtc ttt aga tac tat	2102
Ile Thr Gly Glu Glu Val Cys Glu Lys Tyr Ala Val Phe Arg Tyr Tyr	
545 550 555	
ttc cca agt gtc act tct att gga tgg ttc ctg gat gcg ctt gct ttt	2150
Phe Pro Ser Val Thr Ser Ile Gly Trp Phe Leu Asp Ala Leu Ala Phe	
560 565 570	
cat ctt att att aat tcg aca gga ttt ctt aat ttt gag cac tac cat	2198
His Leu Ile Ile Asn Ser Thr Gly Phe Leu Asn Phe Glu His Tyr His	
575 580 585	
ttt aac caa tta cag gat tat ctg agt caa tct ttt act ttg cat act	2246
Phe Asn Gln Leu Gln Asp Tyr Leu Ser Gln Ser Phe Thr Leu His Thr	
590 595 600 605	
ggg caa gcg att aaa atc agg aag gag att gtt aat agt aca gta tta	2294
Gly Gln Ala Ile Lys Ile Arg Lys Glu Ile Val Asn Ser Thr Val Leu	
610 615 620	
tta tct tca ccg gat atc tgt gtt gaa tta aat cct cct tta ttg att	2342
Leu Ser Ser Pro Asp Ile Cys Val Glu Leu Asn Pro Pro Leu Leu Ile	
625 630 635	
aag aat ggc gat aaa gat tat att cgt att ttc tat tat cga tgt tta	2390
Lys Asn Gly Asp Lys Asp Tyr Ile Arg Ile Phe Tyr Tyr Arg Cys Leu	
640 645 650	
tat gat aaa aaa cct att ttt gta tca aag act tca att atc tct aag	2438
Tyr Asp Lys Lys Pro Ile Phe Val Ser Lys Thr Ser Ile Ile Ser Lys	
655 660 665	
atg aaa taa aaggaaagcg aaatgccaac acaaagtgat attttcactg	2487
Met Lys	
670	
aaataaagaa tagaatatta atgatgaagg atatagaaga tgaagaaata acaccagagt	2547
cctcttttgt ttgccttgaa ttgatagtc ttgactatgt ggaaatccaa gtttttgtgt	2607
tggaagcgta tggattgtg cttaaagccg aacttttttc aaatcattct atttcaacat	2667
taaagagct cactgactat ttaaaatcaa aattgtaatc tgaattttta cttaattatg	2727
ttttttcacc attaacatta agaggttata atg aac gtt tta gaa caa ggt aag	2781
Met Asn Val Leu Glu Gln Gly Lys	
675 680	
ggt gct gct tta tat tca gcc tat tcg gaa aca gaa ggt tct tcg tgg	2829
Val Ala Ala Leu Tyr Ser Ala Tyr Ser Glu Thr Glu Gly Ser Ser Trp	
685 690 695	
gtg gga aac ttg tgc tgt ttt tca agt gat cgg gag cat ttg cct att	2877
Val Gly Asn Leu Cys Cys Phe Ser Ser Asp Arg Glu His Leu Pro Ile	
700 705 710	
atc gtg aat ggg cgt cgt ttc ttg att gaa ttt gtt att cca gat cat	2925
Ile Val Asn Gly Arg Arg Phe Leu Ile Glu Phe Val Ile Pro Asp His	
715 720 725	
tta ctt gat aaa acg gtt aaa ccc aga gta ttc gat ttg gat atc aat	2973
Leu Leu Asp Lys Thr Val Lys Pro Arg Val Phe Asp Leu Asp Ile Asn	

730	735	740	
aaa caa ttt tta ctg cgt cgt gac cat cgt gag ata aat att tat ctt Lys Gln Phe Leu Leu Arg Arg Asp His Arg Glu Ile Asn Ile Tyr Leu 745 750 755 760			3021
tta ggt gaa gga aat ttt atg gat agg acg acg aca gat aaa aat cta Leu Gly Glu Gly Asn Phe Met Asp Arg Thr Thr Asp Lys Asn Leu 765 770 775			3069
ttc gag tta aat gag gat ggt tca cta ttt att aag acg tta cgc cat Phe Glu Leu Asn Glu Asp Gly Ser Leu Phe Ile Lys Thr Leu Arg His 780 785 790			3117
gct ctt ggt aaa tat gtt gct att aat cct tca act acg caa ttt atc Ala Leu Gly Lys Tyr Val Ala Ile Asn Pro Ser Thr Thr Gln Phe Ile 795 800 805			3165
ttc ttt gca caa gga aag tac agt gaa ttt atc atg aat gcc tta aag Phe Phe Ala Gln Gly Lys Tyr Ser Glu Phe Ile Met Asn Ala Leu Lys 810 815 820			3213
aca gtt gaa gac gaa tta tca aaa cgt tat cga gtc aga att att cct Thr Val Glu Asp Glu Leu Ser Lys Arg Tyr Arg Val Arg Ile Ile Pro 825 830 835 840			3261
gaa ttg caa ggg ccg tat tat ggc ttt gaa ctt gat att ctt tct att Glu Leu Gln Gly Pro Tyr Tyr Gly Phe Glu Leu Asp Ile Leu Ser Ile 845 850 855			3309
aca gct taa ttccacaatat tatggagagt gtt atg gaa aag aaa ata aca aca Thr Ala Met Glu Lys Lys Ile Thr Thr 860 865			3362
ttt acc att gag aaa act gat gac aat ttt tat gct aat ggg cgt cat Phe Thr Ile Glu Lys Thr Asp Asp Asn Phe Tyr Ala Asn Gly Arg His 870 875 880			3410
caa tgt atg gta aaa atc tct gta ctt aaa caa gaa tat agg aat ggt Gln Cys Met Val Lys Ile Ser Val Leu Lys Gln Glu Tyr Arg Asn Gly 885 890 895			3458
gat tgg ata aaa tta gca ctt agt gag gct gaa aaa aga tog att cag Asp Trp Ile Lys Leu Ala Leu Ser Glu Ala Glu Lys Arg Ser Ile Gln 900 905 910			3506
gtg gcg gca tta agt gat agc ctc ata tat gac caa tta aaa atg cct Val Ala Ala Leu Ser Asp Ser Leu Ile Tyr Asp Gln Leu Lys Met Pro 915 920 925 930			3554
tca ggt tgg aca acg aca gat gca aga aat aaa ttt gat ctt ggg tta Ser Gly Trp Thr Thr Thr Asp Ala Arg Asn Lys Phe Asp Leu Gly Leu 935 940 945			3602
tta aat ggt gtt tat cat gct gat gct ttt att gac gaa cag gta aca Leu Asn Gly Val Tyr His Ala Asp Ala Phe Ile Asp Glu Gln Val Thr 950 955 960			3650
gat cgt gcg gga gat tgc tgc aca aat gaa aac tat cag aac agt gtg Asp Arg Ala Gly Asp Cys Cys Thr Asn Glu Asn Tyr Gln Asn Ser Val 965 970 975			3698
aaa agt gtt cct gaa att atc tat cgt tat gtc agt agt aat aga aca Lys Ser Val Pro Glu Ile Ile Tyr Arg Tyr Val Ser Ser Asn Arg Thr 980 985 990			3746

agc aca gaa tac cta atg gca aaa atg aca ttt gaa gat acg gat ggg 3794
 Ser Thr Glu Tyr Leu Met Ala Lys Met Thr Phe Glu Asp Thr Asp Gly
 995 1000 1005 1010

aaa cgc aca tta aca acg aat atg tca gtt ggt gat gaa gtt ttt gac 3842
 Lys Arg Thr Leu Thr Asn Met Ser Val Gly Asp Glu Val Phe Asp
 1015 1020 1025

agc aag gtt tta tta aaa gcc att gct cct tat gca att aat aca aat 3890
 Ser Lys Val Leu Leu Lys Ala Ile Ala Pro Tyr Ala Ile Asn Thr Asn
 1030 1035 1040

caa ttg cat gaa aac atc aat aca ttg ttt gat aaa aca gaa gag ccg 3938
 Gln Leu His Glu Asn Ile Asn Thr Leu Phe Asp Lys Thr Glu Glu Pro
 1045 1050 1055

aca aaa tcc gat act cat cat caa ata att aat ctt tat cgc tgg aca 3986
 Thr Lys Ser Asp Thr His His Gln Ile Ile Asn Leu Tyr Arg Trp Thr
 1060 1065 1070

ttg cca tat cat ttg agg att ctt gaa ggg aat gac agt act gtt aat 4034
 Leu Pro Tyr His Leu Arg Ile Leu Glu Gly Asn Asp Ser Thr Val Asn
 1075 1080 1085 1090

aga ata tat gtc ctt ggt aaa gag cca tca aat gat aga ttc ctg aca 4082
 Arg Ile Tyr Val Leu Gly Lys Glu Pro Ser Asn Asp Arg Phe Leu Thr
 1095 1100 1105

aga gga agg gta ttt aaa cga gga act cat atg tga atgcacgtga 4128
 Arg Gly Arg Val Phe Lys Arg Gly Thr His Met
 1110 1115

taatgtgagt ggaggatgtg ttatggacta tgcttatacc gtaactatcc cggacacgca 4188

gcttgctgct gaagtgcctc atgtgacagg gtgttcgtgg acgagtgggtt attatgatgg 4248

atatcatgat gtcacaatca ttgataacta cggttgtcag cataaattta gaattttctc 4308

ggttaatat ggacgtgcgc taagcatagc gagaataagt tgattttcct tagtaaaaaa 4368

cctttgttta tgctggtaaa cgcattgtgcg ttgtccagca attaatatat tccattattg 4428

aaataggaat atagccatat ctgtaattat acataaacga atttttactc gaatataatt 4488

ttaattgatc aaacaggaaa tttaaa atg aaa gct acc gat ata tat tcc aat 4541
 Met Lys Ala Thr Asp Ile Tyr Ser Asn
 1120 1125

gct ttt aat ttc ggt tct tat att aat act ggt gtc gat ccc aga aca 4589
 Ala Phe Asn Phe Gly Ser Tyr Ile Asn Thr Gly Val Asp Pro Arg Thr
 1130 1135 1140

ggt caa tat agt gca aat att aat att atc acg tta aga cct aat aat 4637
 Gly Gln Tyr Ser Ala Asn Ile Asn Ile Ile Thr Leu Arg Pro Asn Asn
 1145 1150 1155

gtg ggt aat tcg gaa caa aca ttg agc cta tca ttc tcg cca tta aca 4685
 Val Gly Asn Ser Glu Gln Thr Leu Ser Leu Ser Phe Ser Pro Leu Thr
 1160 1165 1170 1175

acg tta aac aat ggc ttt ggt att ggc tgg cgc ttt tca tta aca aca 4733
 Thr Leu Asn Asn Gly Phe Gly Ile Gly Trp Arg Phe Ser Leu Thr Thr
 1180 1185 1190

- 7 -

tta gat ata aaa aca ctt aca ttt agc cga gca aat ggg gag caa ttt 4781
 Leu Asp Ile Lys Thr Leu Thr Phe Ser Arg Ala Asn Gly Glu Gln Phe
 1195 1200 1205

aaa tgt aag cca ttg ccg cct aat aat aat gat ctt agt ttt aaa gat 4829
 Lys Cys Lys Pro Leu Pro Pro Asn Asn Asp Leu Ser Phe Lys Asp
 1210 1215 1220

aaa aaa cta aaa gat ttg cgc gta tat aag ctc gat agc aat act ttt 4877
 Lys Lys Leu Lys Asp Leu Arg Val Tyr Lys Leu Asp Ser Asn Thr Phe
 1225 1230 1235

tat gtt tat aac aaa aac ggc att ata gag ata ctt aaa cga att ggg 4925
 Tyr Val Tyr Asn Lys Asn Gly Ile Ile Glu Ile Leu Lys Arg Ile Gly
 1240 1245 1250 1255

tcg agt gat att gca aaa aca gtt gca ctt gaa ttt cct gat ggt gaa 4973
 Ser Ser Asp Ile Ala Lys Thr Val Ala Leu Glu Phe Pro Asp Gly Glu
 1260 1265 1270

gca ttt gat tta att tat aat tca aga ttt gca ttg tcc gaa ata aaa 5021
 Ala Phe Asp Leu Ile Tyr Asn Ser Arg Phe Ala Leu Ser Glu Ile Lys
 1275 1280 1285

tac cgt gtg aca ggt aaa act tat ctt aaa ctc aat tac tct gga aat 5069
 Tyr Arg Val Thr Gly Lys Thr Tyr Leu Lys Leu Asn Tyr Ser Gly Asn
 1290 1295 1300

aac tgt aca tca gtg gaa tac cct gat gat aat aat att tct gcg aaa 5117
 Asn Cys Thr Ser Val Glu Tyr Pro Asp Asp Asn Asn Ile Ser Ala Lys
 1305 1310 1315

ata gca ttc gat tat cgt aac gat tac ctt att acg gtg act gta cct 5165
 Ile Ala Phe Asp Tyr Arg Asn Asp Tyr Leu Ile Thr Val Thr Val Pro
 1320 1325 1330 1335

tac gat gct tct ggt cct att gat tct gcc cga ttt aag atg acc tat 5213
 Tyr Asp Ala Ser Gly Pro Ile Asp Ser Ala Arg Phe Lys Met Thr Tyr
 1340 1345 1350

cag aca tta aaa ggc gta ttt cca gtt atc agc acc ttc cgt aca cca 5261
 Gln Thr Leu Lys Gly Val Phe Pro Val Ile Ser Thr Phe Arg Thr Pro
 1355 1360 1365

acc ggt tat gtt gag ctg gtg agt tat aaa gag aat ggg cat aaa gtg 5309
 Thr Gly Tyr Val Glu Leu Val Ser Tyr Lys Glu Asn Gly His Lys Val
 1370 1375 1380

acg gac acg gaa tat att cct tat gcg gct gca ctc act att caa ccc 5357
 Thr Asp Thr Glu Tyr Ile Pro Tyr Ala Ala Ala Leu Thr Ile Gln Pro
 1385 1390 1395

ggc aat gga caa cct gcg gtc agc aaa tcc tat gaa tat agt tca gta 5405
 Gly Asn Gly Gln Pro Ala Val Ser Lys Ser Tyr Glu Tyr Ser Ser Val
 1400 1405 1410 1415

cat aac ttc ttg ggc tat tct tct ggc cgg aca agc ttt gat tcc agt 5453
 His Asn Phe Leu Gly Tyr Ser Ser Gly Arg Thr Ser Phe Asp Ser Ser
 1420 1425 1430

caa gat aat ttg tat ttg gtc aca ggg aaa tac act tat tca tcc att 5501
 Gln Asp Asn Leu Tyr Leu Val Thr Gly Lys Tyr Thr Tyr Ser Ser Ile
 1435 1440 1445

gaa cgg gtt tta gat ggt caa agt gtg gtt tca gta ata gaa cga gta 5549

Glu Arg Val Leu Asp Gly Gln Ser Val Val Ser Val Ile Glu Arg Val	
1450 1455 1460	
ttt aat aaa ttc cat tta atg acc aaa gaa gca aaa aca caa gat aat	5597
Phe Asn Lys Phe His Leu Met Thr Lys Glu Ala Lys Thr Gln Asp Asn	
1465 1470 1475	
aag aga att aca aca gaa att act tac aat gag gat cta tca aaa agt	5645
Lys Arg Ile Thr Thr Glu Ile Thr Tyr Asn Glu Asp Leu Ser Lys Ser	
1480 1485 1490 1495	
ttc tca gag caa cca gaa aat tta caa caa cct tct cgc gtg tta acc	5693
Phe Ser Glu Gln Pro Glu Asn Leu Gln Gln Pro Ser Arg Val Leu Thr	
1500 1505 1510	
cgt tat acg gat ata caa aca aat act tca cga gaa gag act gtc aat	5741
Arg Tyr Thr Asp Ile Gln Thr Asn Thr Ser Arg Glu Glu Thr Val Asn	
1515 1520 1525	
att aaa agt gat gat tgg gga aat act cta ctt att act gag acc agt	5789
Ile Lys Ser Asp Asp Trp Gly Asn Thr Leu Leu Ile Thr Glu Thr Ser	
1530 1535 1540	
ggg ata cag aaa gaa tac gtt tat tat ccg gtc aat ggc gaa ggt aat	5837
Gly Ile Gln Lys Glu Tyr Val Tyr Pro Val Asn Gly Glu Gly Asn	
1545 1550 1555	
agt tgc cct gcc gat ccc ttg ggt ttt tct cgg ttc tta aaa tca gtt	5885
Ser Cys Pro Ala Asp Pro Leu Gly Phe Ser Arg Phe Leu Lys Ser Val	
1560 1565 1570 1575	
acg caa aaa gga tcg cct gat gct gct caa agt gtc gca aat aaa gtg	5933
Thr Gln Lys Gly Ser Pro Asp Ala Ala Gln Ser Val Ala Asn Lys Val	
1580 1585 1590	
att cat tat aca tat caa aaa ttt cct act ttt acc ggc gct tat gtt	5981
Ile His Tyr Thr Tyr Gln Lys Phe Pro Thr Phe Thr Gly Ala Tyr Val	
1595 1600 1605	
aag gaa tat gtc agt aaa gtc tca gag acg ata gac aat aaa ata gcg	6029
Lys Glu Tyr Val Ser Lys Val Ser Glu Thr Ile Asp Asn Lys Ile Ala	
1610 1615 1620	
aga acc ttt agc tat gtt aac tca ccg acg agt aaa tct cat ggt tcg	6077
Arg Thr Phe Ser Tyr Val Asn Ser Pro Thr Ser Lys Ser His Gly Ser	
1625 1630 1635	
tta gca aaa ata acg tca gtg atg aat aac cag caa acg gtc acc aca	6125
Leu Ala Lys Ile Thr Ser Val Met Asn Asn Gln Gln Thr Val Thr Thr	
1640 1645 1650 1655	
ttt aaa tat gaa tat tca gaa agt gag atg acc aca aat gct acg gtg	6173
Phe Lys Tyr Glu Tyr Ser Glu Ser Glu Met Thr Thr Asn Ala Thr Val	
1660 1665 1670	
acc ggt ttt gat ggc gca cat atg gaa tcg aaa aat gtg acg tct att	6221
Thr Gly Phe Asp Gly Ala His Met Glu Ser Lys Asn Val Thr Ser Ile	
1675 1680 1685	
tat acc cat cgg caa ctt cgt aaa gtt gat gta aac cac gtg att acc	6269
Tyr Thr His Arg Gln Leu Arg Lys Val Asp Val Asn His Val Ile Thr	
1690 1695 1700	
gat cag tct tat gat ctt ttg ggt cgc att aca ggg caa att att gat	6317
Asp Gln Ser Tyr Asp Leu Leu Gly Arg Ile Thr Gly Gln Ile Ile Asp	

1705	1710	1715	
ccc ggc acg gca aga gaa att aaa cgt aat tac gtt tat caa tat ccc Pro Gly Thr Ala Arg Asn Glu Ile Lys Arg Asn Tyr Val Tyr Gln Tyr Pro 1720 1725 1730 1735	6365		
ggc ggt gac gaa aat gat ttt tgg ccg gtg atg ata gaa gtt gat tct Gly Gly Asp Glu Arg Asn Phe Trp Pro Val Met Ile Glu Val Asp Ser 1740 1745 1750	6413		
caa ggc gtc aga cgt aaa acc cat tac gat gga atg gga cgt att tgt Gln Gly Val Arg Lys Thr His Tyr Asp Gly Met Gly Arg Ile Cys 1755 1760 1765	6461		
tcg att gaa gaa caa gat gat gat ggc gcc tgg ggc aca tcg ggg att Ser Ile Glu Glu Gln Asp Asp Gly Ala Trp Gly Thr Ser Gly Ile 1770 1775 1780	6509		
tat caa ggc aca tat cga aaa gtt ctt gcc aga caa tat gat gtt ttg Tyr Gln Gly Thr Tyr Arg Lys Val Leu Ala Arg Gln Tyr Asp Val Leu 1785 1790 1795	6557		
ggg cag ttg agc aag gaa att tca aat gat tgg tta tgg aat tta tct Gly Gln Leu Ser Lys Glu Ile Ser Asn Asp Trp Leu Trp Asn Leu Ser 1800 1805 1810 1815	6605		
gcc aat cct ttg gtt cgt ctt gct acc ccg ttg gtt aca acg aaa acc Ala Asn Pro Leu Val Arg Leu Ala Thr Pro Leu Val Thr Thr Lys Thr 1820 1825 1830	6653		
tat aaa tat gat ggt tgg gga aat ctt tac agc acg gaa tac agt gat Tyr Lys Tyr Asp Gly Trp Gly Asn Leu Tyr Ser Thr Glu Tyr Ser Asp 1835 1840 1845	6701		
ggt cgg ata gag ctg gaa atc cat gat cct att acg agg aca att act Gly Arg Ile Glu Leu Glu Ile His Asp Pro Ile Thr Arg Thr Ile Thr 1850 1855 1860	6749		
caa ggg gtc aaa gga tta ggg atg tta aat att cag caa aat aat ttt Gln Gly Val Lys Gly Leu Gly Met Leu Asn Ile Gln Gln Asn Asn Phe 1865 1870 1875	6797		
gag caa ccg gct tcg atc aaa gct gtg tat cct gat ggt acg ata tat Glu Gln Pro Ala Ser Ile Lys Ala Val Tyr Pro Asp Gly Thr Ile Tyr 1880 1885 1890 1895	6845		
agc acc cgt act tat cgt tat gat gga ttt ggt cgt aca gtg acg gaa Ser Thr Arg Thr Tyr Arg Tyr Asp Gly Phe Gly Arg Thr Val Thr Glu 1900 1905 1910	6893		
aca gat gca gaa ggt cat gct acc caa att gga tat gat gtg ttt gat Thr Asp Ala Glu Gly His Ala Thr Gln Ile Gly Tyr Asp Val Phe Asp 1915 1920 1925	6941		
cgt ata gtg aaa aaa acg ttg cca gac gga aca ata tta gaa tcc gct Arg Ile Val Lys Lys Thr Leu Pro Asp Gly Thr Ile Leu Glu Ser Ala 1930 1935 1940	6989		
tat gca agc ttt agc cat gaa gaa tta att tcg gca ctg aac gtg aat Tyr Ala Ser Phe Ser His Glu Glu Leu Ile Ser Ala Leu Asn Val Asn 1945 1950 1955	7037		
ggc aca cag ttg ggg gca tta gtt tat gat ggt ctt ggg cgg gta ata Gly Thr Gln Leu Gly Ala Leu Val Tyr Asp Gly Leu Gly Arg Val Ile 1960 1965 1970 1975	7085		

agt gat acg gtg ggt ggt cgc aaa acg gaa tat tta tat ggg cct caa Ser Asp Thr Val Gly Gly Arg Lys Thr Glu Tyr Leu Tyr Gly Pro Gln 1980 1985 1990	7133
ggg gac aaa ccg att cag tca att act cct tcg cat aat aag caa aat Gly Asp Lys Pro Ile Gln Ser Ile Thr Pro Ser His Asn Lys Gln Asn 1995 2000 2005	7181
atg gat tac ctc tac tat ctt ggt agt gtg atg tcc aaa ttt acc acg Met Asp Tyr Leu Tyr Tyr Leu Gly Ser Val Met Ser Lys Phe Thr Thr 2010 2015 2020	7229
ggg aca gac caa caa aac ttt cgt tat cat tcg aaa acg gga aca tta Gly Thr Asp Gln Gln Asn Phe Arg Tyr His Ser Lys Thr Gly Thr Leu 2025 2030 2035	7277
tta tct gcg tca gaa ggc gta tct cag act aat tac agt tat ttc cca Leu Ser Ala Ser Glu Gly Val Ser Gln Thr Asn Tyr Ser Tyr Phe Pro 2040 2045 2050 2055	7325
tcg ggt gta tta cag cga gaa tca ttt tta cgg gat aat aaa ccg att Ser Gly Val Leu Gln Arg Glu Ser Phe Leu Arg Asp Asn Lys Pro Ile 2060 2065 2070	7373
tca tcg ggc gag tac ctt tat acg atg tcc ggt ttg att caa cgt cat Ser Ser Gly Glu Tyr Leu Tyr Thr Met Ser Gly Leu Ile Gln Arg His 2075 2080 2085	7421
aaa gat agt ttt ggt cat aat cat gtt tat agt tac gat gct cag gga Lys Asp Ser Phe Gly His Asn His Val Tyr Ser Tyr Asp Ala Gln Gly 2090 2095 2100	7469
aga ttg gtc aaa aca gaa cag gat gca caa tac gct aca ttt gaa tat Arg Leu Val Lys Thr Glu Gln Asp Ala Gln Tyr Ala Thr Phe Glu Tyr 2105 2110 2115	7517
gac aat gtt ggg cga ttg ata aca acg acg acc aaa gac acg acg tca Asp Asn Val Gly Arg Leu Ile Thr Thr Thr Lys Asp Thr Thr Ser 2120 2125 2130 2135	7565
tta tcc caa tta gtg aca aaa atc gaa tat gat gct ttt gat cga gaa Leu Ser Gln Leu Val Thr Lys Ile Glu Tyr Asp Ala Phe Asp Arg Glu 2140 2145 2150	7613
ata aaa cgc tcg cta att agt gac ttc tca ata caa gtt att acc tta Ile Lys Arg Ser Leu Ile Ser Asp Phe Ser Ile Gln Val Ile Thr Leu 2155 2160 2165	7661
agc tat acg aag aat aat caa atc agt caa cgt atc acc tcc atc gat Ser Tyr Thr Lys Asn Asn Gln Ile Ser Gln Arg Ile Thr Ser Ile Asp 2170 2175 2180	7709
ggg gtg gtt atg aaa aat gaa cgt tat caa tat gat aat aat caa cgc Gly Val Val Met Lys Asn Glu Arg Tyr Gln Tyr Asp Asn Asn Gln Arg 2185 2190 2195	7757
tta agc caa tac caa tgt gag gga gaa caa tct ccg att gat cat acg Leu Ser Gln Tyr Gln Cys Glu Gly Glu Gln Ser Pro Ile Asp His Thr 2200 2205 2210 2215	7805
ggg cgt gta tta aat cag cag att tac cat tat gac caa tgg gga aat Gly Arg Val Leu Asn Gln Gln Ile Tyr His Tyr Asp Gln Trp Gly Asn 2220 2225 2230	7853

att aag cgg ctc gat aat aca tat cga gat ggt aag gaa acg gtg gat 7901
 Ile Lys Arg Leu Asp Asn Thr Tyr Arg Asp Gly Lys Glu Thr Val Asp
 2235 2240 2245

tat cat ttc agt caa gcc gat cca act caa ctt att cgt att acc agc 7949
 Tyr His Phe Ser Gln Ala Asp Pro Thr Gln Leu Ile Arg Ile Thr Ser
 2250 2255 2260

gac aaa cag cag ata gag tta agt tat gat gct aat ggc aac cta aca 7997
 Asp Lys Gln Gln Ile Glu Leu Ser Tyr Asp Ala Asn Gly Asn Leu Thr
 2265 2270 2275

cgt gac gaa aaa ggg caa acg ctc att tac gat cag aat aat cgc ttg 8045
 Arg Asp Glu Lys Gly Gln Thr Leu Ile Tyr Asp Gln Asn Asn Arg Leu
 2280 2285 2290 2295

gta cag gtc aaa gac cgg ttg ggc aat ctg gtg tgc agc tac cag tat 8093
 Val Gln Val Lys Asp Arg Leu Gly Asn Leu Val Cys Ser Tyr Gln Tyr
 2300 2305 2310

gat gca ttg aac aaa tta acc gca cag gtt ttg gcg aat ggt acc gtt 8141
 Asp Ala Leu Asn Lys Leu Thr Ala Gln Val Leu Ala Asn Gly Thr Val
 2315 2320 2325

aat cga cag cat tat gct tcc ggt aaa gtg acg aat att caa ttg ggt 8189
 Asn Arg Gln His Tyr Ala Ser Gly Lys Val Thr Asn Ile Gln Leu Gly
 2330 2335 2340

gat gaa gcg att act tgg ttg agc agt gat aag caa cga att gga cat 8237
 Asp Glu Ala Ile Thr Trp Leu Ser Ser Asp Lys Gln Arg Ile Gly His
 2345 2350 2355

caa agc gcc aag aat ggt caa tca gtc tac tat caa tat ggt att gac 8285
 Gln Ser Ala Lys Asn Gly Gln Ser Val Tyr Tyr Gln Tyr Gly Ile Asp
 2360 2365 2370 2375

cat aac agt acg gtt atc gcc agt cag aac gaa aac gag ttg atg gct 8333
 His Asn Ser Thr Val Ile Ala Ser Gln Asn Glu Asn Glu Leu Met Ala
 2380 2385 2390

tta tcc tat aca cct tat ggc ttt agg agt tta att tcc tca tta cgg 8381
 Leu Ser Tyr Thr Pro Tyr Gly Phe Arg Ser Leu Ile Ser Ser Leu Pro
 2395 2400 2405

ggt ttg aat ggc gca cag gtt gat cca gta aca ggc tgg tac ttc tta 8429
 Gly Leu Asn Gly Ala Gln Val Asp Pro Val Thr Gly Trp Tyr Phe Leu
 2410 2415 2420

ggt aac gga tat cgt gtt ttc aac ccg gtt ctc atg agg ttt cac agc 8477
 Gly Asn Gly Tyr Arg Val Phe Asn Pro Val Leu Met Arg Phe His Ser
 2425 2430 2435

ccc gat agt tgg agt cct ttt ggt cgg gga ggg att aac cct tat acc 8525
 Pro Asp Ser Trp Ser Pro Phe Gly Arg Gly Gly Ile Asn Pro Tyr Thr
 2440 2445 2450 2455

tat tgc caa ggc gat ccc ata aac cgg att gat ctg aac ggt cat ctt 8573
 Tyr Cys Gln Gly Asp Pro Ile Asn Arg Ile Asp Leu Asn Gly His Leu
 2460 2465 2470

agt gcc ggc ggg ata tta ggc att gtg cta ggg gca att ggc atc att 8621
 Ser Ala Gly Gly Ile Leu Gly Ile Val Leu Gly Ala Ile Gly Ile Ile
 2475 2480 2485

gtc ggg att gta tca ctg gga gcc gga gcg gcg att agc gcg ggt ctc 8669

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Val Gly Ile Val Ser Leu Gly Ala Gly Ala Ala Ile Ser Ala Gly Leu
 2490 2495 2500
 att gct gcg ggg ggc gct ttg ggg gcg att gct tct acc agc gcg ctt 8717
 Ile Ala Ala Gly Gly Ala Leu Gly Ala Ile Ala Ser Thr Ser Ala Leu
 2505 2510 2515
 gca gtt act gcg act gtc att gga ttg gct gcc gat tcg ata ggg att 8765
 Ala Val Thr Ala Thr Val Ile Gly Leu Ala Ala Asp Ser Ile Gly Ile
 2520 2525 2530 2535
 gcg tca gca gca tta tcg gaa aaa gat cgg aaa aca tct ggg ata tta 8813
 Ala Ser Ala Ala Leu Ser Glu Lys Asp Pro Lys Thr Ser Gly Ile Leu
 2540 2545 2550
 aat tgg att agt gcg gga ttg ggg gtt tta agc ttt ggt atc agc gca 8861
 Asn Trp Ile Ser Ala Gly Leu Gly Val Leu Ser Phe Gly Ile Ser Ala
 2555 2560 2565
 ata acc ttt acc tct tcg ctg gta aaa tcg gca cgg agt ggt tct cag 8909
 Ile Thr Phe Thr Ser Ser Leu Val Lys Ser Ala Arg Ser Gly Ser Gln
 2570 2575 2580
 gca gtc agc gcg ggt gtt atc ggg tca gtg cct ctt gaa ttt ggt gaa 8957
 Ala Val Ser Ala Gly Val Ile Gly Ser Val Pro Leu Glu Phe Gly Glu
 2585 2590 2595
 gtt gct agc cgt tcc agc aga cga tgg gat att gcg tta tct tcg ata 9005
 Val Ala Ser Arg Ser Ser Arg Arg Trp Asp Ile Ala Leu Ser Ser Ile
 2600 2605 2610 2615
 tcg ttg ggc gca aat gcg gcg tct ctc tct acg ggg ata gcg gcg gcg 9053
 Ser Leu Gly Ala Asn Ala Ala Ser Leu Ser Thr Gly Ile Ala Ala Ala
 2620 2625 2630
 gcg gtt gca gac agt aat gcg aat gca gct aat att ctg gga tgg gta 9101
 Ala Val Ala Asp Ser Asn Ala Asn Ala Ala Asn Ile Leu Gly Trp Val
 2635 2640 2645
 tcc ttt ggt ttt ggt gca gta tcg aca acc tca gga ata att gag ctt 9149
 Ser Phe Gly Phe Gly Ala Val Ser Thr Thr Ser Gly Ile Ile Glu Leu
 2650 2655 2660
 acg cgt aca gct tat gca gtg aat cat cag act tgg gaa ctg agt tca 9197
 Thr Arg Thr Ala Tyr Ala Val Asn His Gln Thr Trp Glu Leu Ser Ser
 2665 2670 2675
 tca gca ggt act tcg gag gaa gtg aag cct ata cgt tgt ctc gtt tca 9245
 Ser Ala Gly Thr Ser Glu Glu Val Lys Pro Ile Arg Cys Leu Val Ser
 2680 2685 2690 2695
 cac cgc tgg aat cag aag cag tga atgttaaccc tctcgggca gttgagttaa 9299
 His Arg Trp Asn Gln Lys Gln
 2700
 tcaaacgttt cgaaatagta ccgggaacta tttagccaat cgtccattga aaccgtaat 9359
 gtgttgcgac gtcgtttgac aatataaaga ttctgcgaac cgatttggtta agtctcacga 9419
 aaaataacta ttaggcgaca ttgctgcgc cttttttaag gaactttatc aggttacatt 9479
 tataagaagc tattttgttt tcgacggatg ttggtttctc tgagataaaa aatagaggga 9539
 aatgatgtca aggggtgataa tggtaattg taaaatatgt gatattattc gcatttatat 9599

gtcaatgtaa ttctctttat tattaattt tattgcattt gctacggaa atgccttat 9659

aattttattt ttaataaatt attatttcat cattaaacta aaataaatta ttctctaga 9717

<210> 2

<211> 417

<212> PRT

<213> Photorhabdus luminescens

<400> 2

Met Gln Arg Ala Gln Arg Val Val Ile Thr Gly Met Gly Ala Val Thr
1 5 10 15

Pro Ile Gly Glu Asp Val Glu Ser Cys Trp Gln Ser Ile Ile Glu Lys
20 25 30

Gln His Arg Phe His Arg Ile Glu Phe Pro Asp Ser Phe Ile Asn Ser
35 40 45

Arg Phe Phe Ser Phe Leu Ala Pro Asn Pro Ser Arg Tyr Gln Leu Leu
50 55 60

Pro Lys Lys Leu Thr His Thr Leu Ser Asp Cys Gly Lys Ala Ala Leu
65 70 75 80

Lys Ala Thr Tyr Gln Ala Phe Thr Gln Ala Phe Gly Val Asn Ile Ser
85 90 95

Pro Val Glu Tyr Tyr Asp Lys Tyr Glu Cys Gly Val Ile Leu Gly Ser
100 105 110

Gly Trp Gly Ala Ile Asp Asn Ala Gly Asp His Ala Cys Gln Tyr Lys
115 120 125

Gln Ala Lys Leu Ala His Pro Met Ser Asn Leu Ile Thr Met Pro Ser
130 135 140

Ser Met Thr Ala Ala Cys Ser Ile Met Tyr Gly Leu Arg Gly Tyr Gln
145 150 155 160

Asn Thr Val Met Ala Ala Cys Ala Thr Gly Thr Met Ala Ile Gly Asp
165 170 175

Ala Phe Glu Ile Ile Arg Ser Gly Arg Ala Lys Cys Met Ile Ala Gly
180 185 190

Ala Ala Glu Ser Leu Thr Arg Glu Cys Asn Ile Trp Ser Ile Asp Val
195 200 205

Leu Asn Ala Leu Ser Lys Glu Gln Ala Asp Pro Asn Leu Ala Cys Cys
210 215 220

Pro Phe Ser Leu Asp Arg Ser Gly Phe Val Leu Ala Glu Gly Ala Ala
225 230 235 240

Val Val Cys Leu Glu Asn Tyr Asp Ser Ala Ile Ala Arg Gly Ala Thr
245 250 255

Ile Leu Ala Glu Ile Lys Gly Tyr Ala Gln Tyr Ser Asp Ala Val Asn
260 265 270

Leu Thr Arg Pro Thr Glu Asp Ile Glu Pro Lys Ile Leu Ala Ile Thr
275 280 285

Lys Ala Ile Glu Gln Ala Gln Ile Ser Pro Lys Asp Ile Asp Tyr Ile
 290 295 300
 Asn Ala His Gly Thr Ser Thr Pro Leu Asn Asp Leu Tyr Glu Thr Gln
 305 310 315 320
 Ala Ile Lys Ala Ala Leu Gly Gln Tyr Ala Tyr Gln Val Pro Ile Ser
 325 330 335
 Ser Thr Lys Ser Tyr Thr Gly His Leu Ile Ala Ala Ala Gly Ser Phe
 340 345 350
 Glu Thr Ile Val Cys Val Lys Ala Leu Ala Glu Asn Cys Leu Pro Ala
 355 360 365
 Thr Leu Asn Leu His Arg Ala Asp Pro Asp Cys Asp Leu Asn Tyr Leu
 370 375 380
 Pro Asn Gln His Cys Tyr Thr Ala Gln Pro Glu Val Thr Leu Asn Ile
 385 390 395 400
 Ser Ala Gly Phe Gly Gly His Asn Ala Ala Leu Val Ile Ala Lys Val
 405 410 415

Arg

<210> 3
 <211> 253
 <212> PRT
 <213> Photorhabdus luminescens

<400> 3
 Met Glu Asp Ile Glu His Trp Ser Asn Phe Ser Gly Asp Phe Asn Pro
 1 5 10 15
 Ile His Tyr Ser Ala Lys Ser Glu Ser Leu Arg Asn Ile Gln Gln His
 20 25 30
 Pro Val Gln Gly Met Leu Ser Leu Leu Tyr Val Arg Gln Gln Phe Ser
 35 40 45
 Gln Leu Thr Ser Ala Phe Thr Thr Gly Ile Leu Asn Ile Asp Ala Ser
 50 55 60
 Phe Arg Gln Tyr Val Tyr Thr Ala Leu Pro His Gln Leu Arg Ile Asn
 65 70 75 80
 Thr Lys Asn Lys Thr Phe Lys Leu Glu Asn Pro Ser Lys Glu Asn Thr
 85 90 95
 Leu Phe Gly Asn Thr Ser Val Glu Asn Thr Met Glu Ser Ile Glu Asp
 100 105 110
 Trp Ile Val Gln Asp Asn Cys Gln Lys Leu Thr Ile Thr Gly Glu Glu
 115 120 125
 Val Cys Glu Lys Tyr Ala Val Phe Arg Tyr Tyr Phe Pro Ser Val Thr
 130 135 140
 Ser Ile Gly Trp Phe Leu Asp Ala Leu Ala Phe His Leu Ile Ile Asn
 145 150 155 160
 Ser Thr Gly Phe Leu Asn Phe Glu His Tyr His Phe Asn Gln Leu Gln
 165 170 175

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Asp Tyr Leu Ser Gln Ser Phe Thr Leu His Thr Gly Gln Ala Ile Lys
 180 185 190

Ile Arg Lys Glu Ile Val Asn Ser Thr Val Leu Leu Ser Ser Pro Asp
 195 200 205

Ile Cys Val Glu Leu Asn Pro Pro Leu Leu Ile Lys Asn Gly Asp Lys
 210 215 220

Asp Tyr Ile Arg Ile Phe Tyr Tyr Arg Cys Leu Tyr Asp Lys Lys Pro
 225 230 235 240

Ile Phe Val Ser Lys Thr Ser Ile Ile Ser Lys Met Lys
 245 250

<210> 4

<211> 186

<212> PRT

<213> Photorhabdus luminescens

<400> 4

Met Asn Val Leu Glu Gln Gly Lys Val Ala Ala Leu Tyr Ser Ala Tyr
 1 5 10 15

Ser Glu Thr Glu Gly Ser Ser Trp Val Gly Asn Leu Cys Cys Phe Ser
 20 25 30

Ser Asp Arg Glu His Leu Pro Ile Ile Val Asn Gly Arg Arg Phe Leu
 35 40 45

Ile Glu Phe Val Ile Pro Asp His Leu Leu Asp Lys Thr Val Lys Pro
 50 55 60

Arg Val Phe Asp Leu Asp Ile Asn Lys Gln Phe Leu Leu Arg Arg Asp
 65 70 75 80

His Arg Glu Ile Asn Ile Tyr Leu Leu Gly Glu Gly Asn Phe Met Asp
 85 90 95

Arg Thr Thr Thr Asp Lys Asn Leu Phe Glu Leu Asn Glu Asp Gly Ser
 100 105 110

Leu Phe Ile Lys Thr Leu Arg His Ala Leu Gly Lys Tyr Val Ala Ile
 115 120 125

Asn Pro Ser Thr Thr Gln Phe Ile Phe Phe Ala Gln Gly Lys Tyr Ser
 130 135 140

Glu Phe Ile Met Asn Ala Leu Lys Thr Val Glu Asp Glu Leu Ser Lys
 145 150 155 160

Arg Tyr Arg Val Arg Ile Ile Pro Glu Leu Gln Gly Pro Tyr Tyr Gly
 165 170 175

Phe Glu Leu Asp Ile Leu Ser Ile Thr Ala
 180 185

<210> 5

<211> 258

<212> PRT

<213> Photorhabdus luminescens

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<400> 5

Met Glu Lys Lys Ile Thr Thr Phe Thr Ile Glu Lys Thr Asp
 1 5 10
 Asp Asn Phe Tyr Ala Asn Gly Arg His Gln Cys Met Val Lys Ile Ser
 15 20 25 30
 Val Leu Lys Gln Glu Tyr Arg Asn Gly Asp Trp Ile Lys Leu Ala Leu
 35 40 45
 Ser Glu Ala Glu Lys Arg Ser Ile Gln Val Ala Ala Leu Ser Asp Ser
 50 55 60
 Leu Ile Tyr Asp Gln Leu Lys Met Pro Ser Gly Trp Thr Thr Thr Asp
 65 70 75
 Ala Arg Asn Lys Phe Asp Leu Gly Leu Leu Asn Gly Val Tyr His Ala
 80 85 90
 Asp Ala Phe Ile Asp Glu Gln Val Thr Asp Arg Ala Gly Asp Cys Cys
 95 100 105 110
 Thr Asn Glu Asn Tyr Gln Asn Ser Val Lys Ser Val Pro Glu Ile Ile
 115 120 125
 Tyr Arg Tyr Val Ser Ser Asn Arg Thr Ser Thr Glu Tyr Leu Met Ala
 130 135 140
 Lys Met Thr Phe Glu Asp Thr Asp Gly Lys Arg Thr Leu Thr Thr Asn
 145 150 155
 Met Ser Val Gly Asp Glu Val Phe Asp Ser Lys Val Leu Leu Lys Ala
 160 165 170
 Ile Ala Pro Tyr Ala Ile Asn Thr Asn Gln Leu His Glu Asn Ile Asn
 175 180 185 190
 Thr Leu Phe Asp Lys Thr Glu Glu Pro Thr Lys Ser Asp Thr His His
 195 200 205
 Gln Ile Ile Asn Leu Tyr Arg Trp Thr Leu Pro Tyr His Leu Arg Ile
 210 215 220
 Leu Glu Gly Asn Asp Ser Thr Val Asn Arg Ile Tyr Val Leu Gly Lys
 225 230 235
 Glu Pro Ser Asn Asp Arg Phe Leu Thr Arg Gly Arg Val Phe Lys Arg
 240 245 250
 Gly Thr His Met
 255

<210> 6

<211> 1584

<212> PRT

<213> Photorhabdus luminescens

<400> 6

Met Lys Ala Thr Asp Ile Tyr Ser Asn Ala Phe Asn Phe Gly Ser Tyr
 1 5 10 15
 Ile Asn Thr Gly Val Asp Pro Arg Thr Gly Gln Tyr Ser Ala Asn Ile
 20 25 30

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Asn Ile Ile Thr Leu Arg Pro Asn Asn Val Gly Asn Ser Glu Gln Thr
 35 40 45
 Leu Ser Leu Ser Phe Ser Pro Leu Thr Thr Leu Asn Asn Gly Phe Gly
 50 55 60
 Ile Gly Trp Arg Phe Ser Leu Thr Thr Leu Asp Ile Lys Thr Leu Thr
 65 70 75 80
 Phe Ser Arg Ala Asn Gly Glu Gln Phe Lys Cys Lys Pro Leu Pro Pro
 85 90 95
 Asn Asn Asn Asp Leu Ser Phe Lys Asp Lys Lys Leu Lys Asp Leu Arg
 100 105 110
 Val Tyr Lys Leu Asp Ser Asn Thr Phe Tyr Val Tyr Asn Lys Asn Gly
 115 120 125
 Ile Ile Glu Ile Leu Lys Arg Ile Gly Ser Ser Asp Ile Ala Lys Thr
 130 135 140
 Val Ala Leu Glu Phe Pro Asp Gly Glu Ala Phe Asp Leu Ile Tyr Asn
 145 150 155 160
 Ser Arg Phe Ala Leu Ser Glu Ile Lys Tyr Arg Val Thr Gly Lys Thr
 165 170 175
 Tyr Leu Lys Leu Asn Tyr Ser Gly Asn Asn Cys Thr Ser Val Glu Tyr
 180 185 190
 Pro Asp Asp Asn Asn Ile Ser Ala Lys Ile Ala Phe Asp Tyr Arg Asn
 195 200 205
 Asp Tyr Leu Ile Thr Val Thr Val Pro Tyr Asp Ala Ser Gly Pro Ile
 210 215 220
 Asp Ser Ala Arg Phe Lys Met Thr Tyr Gln Thr Leu Lys Gly Val Phe
 225 230 235 240
 Pro Val Ile Ser Thr Phe Arg Thr Pro Thr Gly Tyr Val Glu Leu Val
 245 250 255
 Ser Tyr Lys Glu Asn Gly His Lys Val Thr Asp Thr Glu Tyr Ile Pro
 260 265 270
 Tyr Ala Ala Ala Leu Thr Ile Gln Pro Gly Asn Gly Gln Pro Ala Val
 275 280 285
 Ser Lys Ser Tyr Glu Tyr Ser Ser Val His Asn Phe Leu Gly Tyr Ser
 290 295 300
 Ser Gly Arg Thr Ser Phe Asp Ser Ser Gln Asp Asn Leu Tyr Leu Val
 305 310 315 320
 Thr Gly Lys Tyr Thr Tyr Ser Ser Ile Glu Arg Val Leu Asp Gly Gln
 325 330 335
 Ser Val Val Ser Val Ile Glu Arg Val Phe Asn Lys Phe His Leu Met
 340 345 350
 Thr Lys Glu Ala Lys Thr Gln Asp Asn Lys Arg Ile Thr Thr Glu Ile
 355 360 365
 Thr Tyr Asn Glu Asp Leu Ser Lys Ser Phe Ser Glu Gln Pro Glu Asn
 370 375 380

Leu Gln Gln Pro Ser Arg Val Leu Thr Arg Tyr Thr Asp Ile Gln Thr
 385 390 395 400
 Asn Thr Ser Arg Glu Glu Thr Val Asn Ile Lys Ser Asp Asp Trp Gly
 405 410 415
 Asn Thr Leu Leu Ile Thr Glu Thr Ser Gly Ile Gln Lys Glu Tyr Val
 420 425 430
 Tyr Tyr Pro Val Asn Gly Glu Gly Asn Ser Cys Pro Ala Asp Pro Leu
 435 440 445
 Gly Phe Ser Arg Phe Leu Lys Ser Val Thr Gln Lys Gly Ser Pro Asp
 450 455 460
 Ala Ala Gln Ser Val Ala Asn Lys Val Ile His Tyr Thr Tyr Gln Lys
 465 470 475 480
 Phe Pro Thr Phe Thr Gly Ala Tyr Val Lys Glu Tyr Val Ser Lys Val
 485 490 495
 Ser Glu Thr Ile Asp Asn Lys Ile Ala Arg Thr Phe Ser Tyr Val Asn
 500 505 510
 Ser Pro Thr Ser Lys Ser His Gly Ser Leu Ala Lys Ile Thr Ser Val
 515 520 525
 Met Asn Asn Gln Gln Thr Val Thr Thr Phe Lys Tyr Glu Tyr Ser Glu
 530 535 540
 Ser Glu Met Thr Thr Asn Ala Thr Val Thr Gly Phe Asp Gly Ala His
 545 550 555 560
 Met Glu Ser Lys Asn Val Thr Ser Ile Tyr Thr His Arg Gln Leu Arg
 565 570 575
 Lys Val Asp Val Asn His Val Ile Thr Asp Gln Ser Tyr Asp Leu Leu
 580 585 590
 Gly Arg Ile Thr Gly Gln Ile Ile Asp Pro Gly Thr Ala Arg Glu Ile
 595 600 605
 Lys Arg Asn Tyr Val Tyr Gln Tyr Pro Gly Gly Asp Glu Asn Asp Phe
 610 615 620
 Trp Pro Val Met Ile Glu Val Asp Ser Gln Gly Val Arg Arg Lys Thr
 625 630 635 640
 His Tyr Asp Gly Met Gly Arg Ile Cys Ser Ile Glu Glu Gln Asp Asp
 645 650 655
 Asp Gly Ala Trp Gly Thr Ser Gly Ile Tyr Gln Gly Thr Tyr Arg Lys
 660 665 670
 Val Leu Ala Arg Gln Tyr Asp Val Leu Gly Gln Leu Ser Lys Glu Ile
 675 680 685
 Ser Asn Asp Trp Leu Trp Asn Leu Ser Ala Asn Pro Leu Val Arg Leu
 690 695 700
 Ala Thr Pro Leu Val Thr Thr Lys Thr Tyr Lys Tyr Asp Gly Trp Gly
 705 710 715 720
 Asn Leu Tyr Ser Thr Glu Tyr Ser Asp Gly Arg Ile Glu Leu Glu Ile

725										730					735				
His	Asp	Pro	Ile	Thr	Arg	Thr	Ile	Thr	Gln	Gly	Val	Lys	Gly	Leu	Gly				
			740						745					750					
Met	Leu	Asn	Ile	Gln	Gln	Asn	Asn	Phe	Glu	Gln	Pro	Ala	Ser	Ile	Lys				
		755					760						765						
Ala	Val	Tyr	Pro	Asp	Gly	Thr	Ile	Tyr	Ser	Thr	Arg	Thr	Tyr	Arg	Tyr				
	770					775					780								
Asp	Gly	Phe	Gly	Arg	Thr	Val	Thr	Glu	Thr	Asp	Ala	Glu	Gly	His	Ala				
785					790					795					800				
Thr	Gln	Ile	Gly	Tyr	Asp	Val	Phe	Asp	Arg	Ile	Val	Lys	Lys	Thr	Leu				
			805						810					815					
Pro	Asp	Gly	Thr	Ile	Leu	Glu	Ser	Ala	Tyr	Ala	Ser	Phe	Ser	His	Glu				
			820					825					830						
Glu	Leu	Ile	Ser	Ala	Leu	Asn	Val	Asn	Gly	Thr	Gln	Leu	Gly	Ala	Leu				
	835					840						845							
Val	Tyr	Asp	Gly	Leu	Gly	Arg	Val	Ile	Ser	Asp	Thr	Val	Gly	Gly	Arg				
	850					855					860								
Lys	Thr	Glu	Tyr	Leu	Tyr	Gly	Pro	Gln	Gly	Asp	Lys	Pro	Ile	Gln	Ser				
865					870					875					880				
Ile	Thr	Pro	Ser	His	Asn	Lys	Gln	Asn	Met	Asp	Tyr	Leu	Tyr	Tyr	Leu				
			885						890					895					
Gly	Ser	Val	Met	Ser	Lys	Phe	Thr	Thr	Gly	Thr	Asp	Gln	Gln	Asn	Phe				
		900						905					910						
Arg	Tyr	His	Ser	Lys	Thr	Gly	Thr	Leu	Leu	Ser	Ala	Ser	Glu	Gly	Val				
	915					920						925							
Ser	Gln	Thr	Asn	Tyr	Ser	Tyr	Phe	Pro	Ser	Gly	Val	Leu	Gln	Arg	Glu				
	930					935					940								
Ser	Phe	Leu	Arg	Asp	Asn	Lys	Pro	Ile	Ser	Ser	Gly	Glu	Tyr	Leu	Tyr				
945					950					955					960				
Thr	Met	Ser	Gly	Leu	Ile	Gln	Arg	His	Lys	Asp	Ser	Phe	Gly	His	Asn				
			965						970					975					
His	Val	Tyr	Ser	Tyr	Asp	Ala	Gln	Gly	Arg	Leu	Val	Lys	Thr	Glu	Gln				
		980						985					990						
Asp	Ala	Gln	Tyr	Ala	Thr	Phe	Glu	Tyr	Asp	Asn	Val	Gly	Arg	Leu	Ile				
	995					1000						1005							
Thr	Thr	Thr	Thr	Lys	Asp	Thr	Thr	Ser	Leu	Ser	Gln	Leu	Val	Thr	Lys				
	1010					1015					1020								
Ile	Glu	Tyr	Asp	Ala	Phe	Asp	Arg	Glu	Ile	Lys	Arg	Ser	Leu	Ile	Ser				
025				1030						1035					1040				
Asp	Phe	Ser	Ile	Gln	Val	Ile	Thr	Leu	Ser	Tyr	Thr	Lys	Asn	Asn	Gln				
			1045					1050					1055						
Ile	Ser	Gln	Arg	Ile	Thr	Ser	Ile	Asp	Gly	Val	Val	Met	Lys	Asn	Glu				
	1060						1065						1070						

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Arg Tyr Gln Tyr Asp Asn Asn Gln Arg Leu Ser Gln Tyr Gln Cys Glu
 1075 1080 1085
 Gly Glu Gln Ser Pro Ile Asp His Thr Gly Arg Val Leu Asn Gln Gln
 1090 1095 1100
 Ile Tyr His Tyr Asp Gln Trp Gly Asn Ile Lys Arg Leu Asp Asn Thr
 105 1110 1115 1120
 Tyr Arg Asp Gly Lys Glu Thr Val Asp Tyr His Phe Ser Gln Ala Asp
 1125 1130 1135
 Pro Thr Gln Leu Ile Arg Ile Thr Ser Asp Lys Gln Gln Ile Glu Leu
 1140 1145 1150
 Ser Tyr Asp Ala Asn Gly Asn Leu Thr Arg Asp Glu Lys Gly Gln Thr
 1155 1160 1165
 Leu Ile Tyr Asp Gln Asn Asn Arg Leu Val Gln Val Lys Asp Arg Leu
 1170 1175 1180
 Gly Asn Leu Val Cys Ser Tyr Gln Tyr Asp Ala Leu Asn Lys Leu Thr
 185 1190 1195 1200
 Ala Gln Val Leu Ala Asn Gly Thr Val Asn Arg Gln His Tyr Ala Ser
 1205 1210 1215
 Gly Lys Val Thr Asn Ile Gln Leu Gly Asp Glu Ala Ile Thr Trp Leu
 1220 1225 1230
 Ser Ser Asp Lys Gln Arg Ile Gly His Gln Ser Ala Lys Asn Gly Gln
 1235 1240 1245
 Ser Val Tyr Tyr Gln Tyr Gly Ile Asp His Asn Ser Thr Val Ile Ala
 1250 1255 1260
 Ser Gln Asn Glu Asn Glu Leu Met Ala Leu Ser Tyr Thr Pro Tyr Gly
 265 1270 1275 1280
 Phe Arg Ser Leu Ile Ser Ser Leu Pro Gly Leu Asn Gly Ala Gln Val
 1285 1290 1295
 Asp Pro Val Thr Gly Trp Tyr Phe Leu Gly Asn Gly Tyr Arg Val Phe
 1300 1305 1310
 Asn Pro Val Leu Met Arg Phe His Ser Pro Asp Ser Trp Ser Pro Phe
 1315 1320 1325
 Gly Arg Gly Gly Ile Asn Pro Tyr Thr Tyr Cys Gln Gly Asp Pro Ile
 1330 1335 1340
 Asn Arg Ile Asp Leu Asn Gly His Leu Ser Ala Gly Gly Ile Leu Gly
 345 1350 1355 1360
 Ile Val Leu Gly Ala Ile Gly Ile Ile Val Gly Ile Val Ser Leu Gly
 1365 1370 1375
 Ala Gly Ala Ala Ile Ser Ala Gly Leu Ile Ala Ala Gly Gly Ala Leu
 1380 1385 1390
 Gly Ala Ile Ala Ser Thr Ser Ala Leu Ala Val Thr Ala Thr Val Ile
 1395 1400 1405
 Gly Leu Ala Ala Asp Ser Ile Gly Ile Ala Ser Ala Ala Leu Ser Glu
 1410 1415 1420

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Lys Asp Pro Lys Thr Ser Gly Ile Leu Asn Trp Ile Ser Ala Gly Leu
 425 1430 1435 1440
 Gly Val Leu Ser Phe Gly Ile Ser Ala Ile Thr Phe Thr Ser Ser Leu
 1445 1450 1455
 Val Lys Ser Ala Arg Ser Gly Ser Gln Ala Val Ser Ala Gly Val Ile
 1460 1465 1470
 Gly Ser Val Pro Leu Glu Phe Gly Glu Val Ala Ser Arg Ser Ser Arg
 1475 1480 1485
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Gln	Glu	Ala	Ser	Trp	Thr	Gly	Asp	Asn	Glu	Thr	Val	Trp	Gln	Asn	Met	
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Leu	Ala	Asp	Asp	Ile	Tyr	Thr	Thr	Leu	Ser	Ala	Phe	Asp	Ala	Thr	Gly	
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gct	tta	ctc	act	cag	acc	gat	gcg	aaa	ggg	aac	att	cag	agg	cta	acc	15896
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Tyr	Asp	Val	Ala	Gly	Gln	Leu	Asn	Gly	Ser	Trp	Leu	Thr	Leu	Lys	Asp	
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Gln	Pro	Glu	Gln	Val	Ile	Ile	Arg	Ser	Leu	Thr	Tyr	Ser	Ala	Ala	Gly	
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Tyr	Glu	Pro	Glu	Thr	Gln	Gln	Leu	Ile	Gly	Thr	Lys	Thr	His	Arg	Pro	
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tca	gat	gcc	aaa	gtg	ttg	caa	gat	cta	cgt	tat	gag	tat	gac	cgg	gta	16136
Ser	Asp	Ala	Lys	Val	Leu	Gln	Asp	Leu	Arg	Tyr	Glu	Tyr	Asp	Pro	Val	
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Gly	Asn	Val	Ile	Ser	Ile	Arg	Asn	Asp	Ala	Glu	Ala	Thr	Arg	Phe	Trp	
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cac	aat	cag	aaa	gtg	gcg	cgg	gaa	aac	act	tat	acc	tac	gac	tcc	ttg	16232
His	Asn	Gln	Lys	Val	Ala	Pro	Glu	Asn	Thr	Tyr	Thr	Tyr	Asp	Ser	Leu	
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tat	cag	ctt	atc	agc	gca	acc	ggg	cgc	gag	atg	gcg	aat	ata	ggt	cag	16280
Tyr	Gln	Leu	Ile	Ser	Ala	Thr	Gly	Arg	Glu	Met	Ala	Asn	Ile	Gly	Gln	
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Gln	Ser	Asn	Gln	Leu	Pro	Ser	Leu	Thr	Leu	Pro	Ser	Asp	Asn	Asn	Thr	
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tac	acc	aac	tat	acc	cgt	act	tat	act	tat	gac	cgt	ggc	ggc	aat	ttg	16376
Tyr	Thr	Asn	Tyr	Thr	Arg	Thr	Tyr	Thr	Tyr	Asp	Arg	Gly	Gly	Asn	Leu	
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act	aaa	atc	cag	cac	agt	tca	cgg	gcg	acg	caa	aac	aac	tac	acc	aca	16424
Thr	Lys	Ile	Gln	His	Ser	Ser	Pro	Ala	Thr	Gln	Asn	Asn	Tyr	Thr	Thr	
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aac	atc	acg	gtt	tct	aac	cgg	agc	aat	cgc	gca	gta	ctc	agc	act	ctg	16472
Asn	Ile	Thr	Val	Ser	Asn	Arg	Ser	Asn	Arg	Ala	Val	Leu	Ser	Thr	Leu	

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cag aac acg ttg ata tca gga caa aac ctg aac tgg aat aca cgc ggt Gln Asn Thr Leu Ile Ser Gly Gln Asn Leu Asn Trp Asn Thr Arg Gly 455 460 465			16568
gaa cta caa cat gtg aca ttg gtg aaa cgg gac aag ggc gcc aat gat Glu Leu Gln His Val Thr Leu Val Lys Arg Asp Lys Gly Ala Asn Asp 470 475 480			16616
gat cgg gaa tgg tat cgc tat agt agt gac ggg aga agg ata tta aaa Asp Arg Glu Trp Tyr Arg Tyr Ser Ser Asp Gly Arg Arg Ile Leu Lys 485 490 495			16664
atc aat gaa cag cag acc agc agc aac tct caa aca cag aga ata act Ile Asn Glu Gln Gln Thr Ser Ser Asn Ser Gln Thr Gln Arg Ile Thr 500 505 510			16712
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Gln Ser Thr Thr Tyr Pro Ile Lys Ser Ala Ser Ile Lys Pro Thr Thr	
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 950 955

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960															965	
gag Glu	ata Ile	oct Pro	gat Asp	gta Val	tta Leu	aaa Lys	atc Ile	cag Gln	tgt Cys	ggt Gly	ttt Phe	cag Gln	tgt Cys	ctg Leu	aca Thr	23854
970															975	
gat Asp	att Ile	agc Ser	cac His	agc Ser	tct Ser	ttt Phe	aac Asn	gaa Glu	ttt Phe	cac His	cag Gln	caa Gln	gta Val	tcc Ser	gaa Glu	23902
985															990	
995															1000	
cac His	ctc Leu	tcc Ser	tgg Trp	tcc Ser	gaa Glu	gca Ala	cac His	gac Asp	tta Leu	tat Tyr	cat His	gat Asp	gca Ala	caa Gln	cag Gln	23950
1005															1010	
1015																
gcc Ala	caa Gln	aag Lys	gat Asp	aat Asn	cgg Arg	ctg Leu	tat Tyr	gaa Glu	gcg Ala	cgt Arg	att Ile	ctt Leu	aaa Lys	cgc Arg	acg Thr	23998
1020															1025	
1030																
aat Asn	cct Pro	caa Gln	tta Leu	caa Gln	aat Asn	gct Ala	gta Val	cat His	ctt Leu	gcc Ala	atc Ile	gta Val	gcg Ala	cct Pro	aat Asn	24046
1035															1040	
1045																
gct Ala	gaa Glu	ctg Leu	ata Ile	ggc Gly	tat Tyr	aac Asn	aac Asn	caa Gln	ttt Phe	agc Ser	ggc Gly	agg Arg	gcc Ala	agt Ser	caa Gln	24094
1050															1055	
1060																
tat Tyr	gtc Val	gcg Ala	cgg Pro	ggg Gly	acc Thr	gtt Val	tcc Ser	tcc Ser	atg Met	ttc Phe	tcc Ser	ccc Pro	gcc Ala	gct Ala	tat Tyr	24142
1065															1070	
1075															1080	
ttg Leu	act Thr	gag Glu	ctt Leu	tat Tyr	cgt Arg	gaa Glu	gca Ala	cgc Arg	aat Asn	tta Leu	cac His	gcc Ala	agc Ser	gat Asp	tcc Ser	24190
1085															1090	
1095																
gtt Val	tat Tyr	cgc Arg	ctg Leu	gat Asp	act Thr	cgc Arg	cgc Arg	cca Pro	gat Asp	ctc Leu	aaa Lys	tca Ser	atg Met	gcg Ala	ctc Leu	24238
1100															1105	
1110																
agt Ser	caa Gln	caa Gln	aat Asn	atg Met	gat Asp	acg Thr	gaa Glu	ctt Leu	tcc Ser	act Thr	ctc Leu	tct Ser	tta Leu	tcc Ser	aat Asn	24286
1115															1120	
1125																
gag Glu	cta Leu	tta Leu	ttg Leu	gaa Glu	agc Ser	att Ile	aaa Lys	act Thr	gag Glu	tct Ser	aag Lys	ctg Leu	gat Asp	aat Asn	tat Tyr	24334
1130															1135	
1140																
act Thr	caa Gln	gtg Val	atg Met	gaa Glu	atg Met	ctc Leu	tcc Ser	gct Ala	ttc Phe	cgt Arg	cct Pro	tcc Ser	ggc Gly	gcg Ala	acg Thr	24382
1145															1150	
1155															1160	
cct Pro	tat Tyr	cac His	gat Asp	gct Ala	tac Tyr	gaa Glu	aat Asn	gtg Val	cgt Arg	aaa Lys	gtt Val	atc Ile	cag Gln	cta Leu	caa Gln	24430
1165															1170	
1175																
gat Asp	cct Pro	ggg Gly	ctt Leu	gag Glu	caa Gln	tta Leu	aat Asn	gct Ala	tca Ser	cca Pro	gcc Ala	att Ile	gcc Ala	ggg Gly	ctg Leu	24478
1180															1185	
1190																
atg Met	cat His	caa Gln	gct Ala	tcc Ser	cta Leu	tta Leu	ggt Gly	att Ile	aac Asn	gct Ala	tca Ser	atc Ile	tca Ser	cct Pro	gag Glu	24526
1195															1200	
1205																
ttg Leu	ttt Phe	aat Asn	att Ile	ctg Leu	acg Thr	gag Glu	gag Glu	att Ile	act Thr	gaa Glu	ggt Gly	aat Asn	gct Ala	gag Glu	gaa Glu	24574

1210	1215	1220	
ctt tat aag aaa aat ttt ggt aat atc gaa ccg gct tca ctg gct atg			24622
Leu Tyr Lys Lys Asn Phe Gly Asn Ile Glu Pro Ala Ser Leu Ala Met			
1225	1230	1235	1240
ccg gaa tac ctt aga cgt tat tac aat tta agt gat gaa gaa ctc agc			24670
Pro Glu Tyr Leu Arg Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser			
1245	1250		1255
cag ttt att ggt aaa gcc agc aat ttc ggc caa caa gaa tat agt aat			24718
Gln Phe Ile Gly Lys Ala Ser Asn Phe Gly Gln Gln Glu Tyr Ser Asn			
1260	1265		1270
aac caa ctc att act ccg ata gtc aac agc aat gat ggc aca gtc aag			24766
Asn Gln Leu Ile Thr Pro Ile Val Asn Ser Asn Asp Gly Thr Val Lys			
1275	1280		1285
gta tat cga att acc cgc gaa tat aca aca aat gcc aat caa gta gac			24814
Val Tyr Arg Ile Thr Arg Gly Tyr Thr Thr Asn Ala Asn Gln Val Asp			
1290	1295		1300
gtg gag ctg ttt ccc tac ggt gga gaa aat tat cag tta aat tac aaa			24862
Val Glu Leu Phe Pro Tyr Gly Gly Glu Asn Tyr Gln Leu Asn Tyr Lys			
1305	1310		1315
ttc aaa gat tct cgt cag gat gtc tcc tat tta tcc atc aaa tta aat			24910
Phe Lys Asp Ser Arg Gln Asp Val Ser Tyr Leu Ser Ile Lys Leu Asn			
1325	1330		1335
gac aaa aga gaa ctt atc cga att gaa gga gcg cct cag gtc aac atc			24958
Asp Lys Arg Glu Leu Ile Arg Ile Glu Gly Ala Pro Gln Val Asn Ile			
1340	1345		1350
gaa tat tca gaa cat atc aca tta agt aca act gat atc agt caa cct			25006
Glu Tyr Ser Glu His Ile Thr Leu Ser Thr Thr Asp Ile Ser Gln Pro			
1355	1360		1365
ttt gaa atc ggc cta aca cga gta tat cct tct agt tct tgg gca tat			25054
Phe Glu Ile Gly Leu Thr Arg Val Tyr Pro Ser Ser Ser Trp Ala Tyr			
1370	1375		1380
gca gcc gca aaa ttt acc att gag gaa tat aac caa tac tct ttc ctg			25102
Ala Ala Ala Lys Phe Thr Ile Glu Glu Tyr Asn Gln Tyr Ser Phe Leu			
1385	1390		1395
1400			
tta aaa ctc aat aaa gct att cgt cta tct cgt gcg aca gaa tta tca			25150
Leu Lys Leu Asn Lys Ala Ile Arg Leu Ser Arg Ala Thr Glu Leu Ser			
1405	1410		1415
ccc acc att ctg gaa agt att gtg cgt agt gtt aat cag caa ctg gat			25198
Pro Thr Ile Leu Glu Ser Ile Val Arg Ser Val Asn Gln Gln Leu Asp			
1420	1425		1430
atc aac gca gaa gta tta ggt aaa gtt ttt ctg act aaa tat tat atg			25246
Ile Asn Ala Glu Val Leu Gly Lys Val Phe Leu Thr Lys Tyr Tyr Met			
1435	1440		1445
caa cgt tat gct att aat gct gaa act gcc cta ata cta tgc aat gca			25294
Gln Arg Tyr Ala Ile Asn Ala Glu Thr Ala Leu Ile Leu Cys Asn Ala			
1450	1455		1460
ctt att tca caa cgt tca tat gat aat caa cct agc caa ttt gat cgc			25342
Leu Ile Ser Gln Arg Ser Tyr Asp Asn Gln Pro Ser Gln Phe Asp Arg			
1465	1470		1475
			1480

ctg ttt aat acg cca tta ctg aac ggc caa tat ttt tct acc gga gat Leu Phe Asn Thr Pro Leu Leu Asn Gly Gln Tyr Phe Ser Thr Gly Asp 1485 1490 1495	25390
gaa gag att gat tta aat cca ggt agt act ggc gat tgg cgt aaa tcc Glu Glu Ile Asp Leu Asn Pro Gly Ser Thr Gly Asp Trp Arg Lys Ser 1500 1505 1510	25438
gtg ctt aaa cgt gca ttt aat atc gat gat att tcc ctc tac cgc ctg Val Leu Lys Arg Ala Phe Asn Ile Asp Asp Ile Ser Leu Tyr Arg Leu 1515 1520 1525	25486
ctt aaa att acc aac cat aat aat caa gat gga aag att aaa aat aac Leu Lys Ile Thr Asn His Asn Asn Gln Asp Gly Lys Ile Lys Asn Asn 1530 1535 1540	25534
tta aat aat ctt tct gat tta tat att ggg aaa tta ctg gca gaa att Leu Asn Asn Leu Ser Asp Leu Tyr Ile Gly Lys Leu Leu Ala Glu Ile 1545 1550 1555 1560	25582
cat caa tta acc att gat gaa ttg gat tta ttg ctg gtt gcc gtg ggt His Gln Leu Thr Ile Asp Glu Leu Asp Leu Leu Val Ala Val Gly 1565 1570 1575	25630
gaa gga gaa act aat tta tcc gct atc agt gat aaa caa ctg gcg gca Glu Gly Glu Thr Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Ala 1580 1585 1590	25678
ctg atc aga aaa ctc aat acc att acc gtc tgg cta cag aca cag aag Leu Ile Arg Lys Leu Asn Thr Ile Thr Val Trp Leu Gln Thr Gln Lys 1595 1600 1605	25726
tgg agt gcg ttc caa tta ttt gtt atg act tcc acc agc tat aac aaa Trp Ser Ala Phe Gln Leu Phe Val Met Thr Ser Thr Ser Tyr Asn Lys 1610 1615 1620	25774
acg ctg acg cct gaa att aag aat ctg ctg gat acc gtc tac cac ggt Thr Leu Thr Pro Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly 1625 1630 1635 1640	25822
tta caa ggc ttt gat aaa gac aag gca aat tta ctg cat gtt atg gcg Leu Gln Gly Phe Asp Lys Asp Lys Ala Asn Leu Leu His Val Met Ala 1645 1650 1655	25870
ccc tat att gcg gcc acc tta caa tta tca tcg gaa aat gtc gcc cat Pro Tyr Ile Ala Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His 1660 1665 1670	25918
tct gtg ctg ctt tgg gca gac aag tta aag ccc ggc gac ggc gca atg Ser Val Leu Leu Trp Ala Asp Lys Leu Lys Pro Gly Asp Gly Ala Met 1675 1680 1685	25966
aca gcc gaa aaa ttc tgg gac tgg ttg aat act caa tat acg cca gat Thr Ala Glu Lys Phe Trp Asp Trp Leu Asn Thr Gln Tyr Thr Pro Asp 1690 1695 1700	26014
tca tcg gaa gta tta gca aca cag gaa cat att gtt cag tat tgt cag Ser Ser Glu Val Leu Ala Thr Gln Glu His Ile Val Gln Tyr Cys Gln 1705 1710 1715 1720	26062
gcg ttg gcg caa tta gaa atg gtt tac cat tcc acc ggt atc aat gaa Ala Leu Ala Gln Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu 1725 1730 1735	26110

aac gcc ttc cgc ctg ttt gtg aca aaa cca gag atg ttt ggc tcg tca Asn Ala Phe Arg Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ser Ser 1740 1745 1750	26158
act gag gca gta cct gcg cat gat gca ctt tca ctg atc atg ctg acg Thr Glu Ala Val Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr 1755 1760 1765	26206
cgt ttt gca gat tgg gtt aat gcg tta ggc gaa aaa gcc tct tcc gta Arg Phe Ala Asp Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val 1770 1775 1780	26254
cta gcg gca ttt gaa gct aac agt tta acg gca gaa caa ttg gct gat Leu Ala Ala Phe Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp 1785 1790 1795 1800	26302
gcc atg aat ctt gat gct aat ttg cta ttg caa gcc agt act caa gca Ala Met Asn Leu Asp Ala Asn Leu Leu Leu Gln Ala Ser Thr Gln Ala 1805 1810 1815	26350
caa aac cat caa cat ctt ccc cca gtg acg caa aaa aat gct ttc tcc Gln Asn His Gln His Leu Pro Pro Val Thr Gln Lys Asn Ala Phe Ser 1820 1825 1830	26398
tgt tgg aca tct atc gac act atc ctg caa tgg gtt aat gtt gca caa Cys Trp Thr Ser Ile Asp Thr Ile Leu Gln Trp Val Asn Val Ala Gln 1835 1840 1845	26446
caa ttg aat gtc gcc cca cag gga gtt tcc gct ttg gtc ggg ctg gat Gln Leu Asn Val Ala Pro Gln Gly Val Ser Ala Leu Val Gly Leu Asp 1850 1855 1860	26494
tat att caa tta aat caa aaa atc ccc acc tat gcc cag tgg gaa agt Tyr Ile Gln Leu Asn Gln Lys Ile Pro Thr Tyr Ala Gln Trp Glu Ser 1865 1870 1875 1880	26542
gct ggg gaa ata ttg act gcc gga ttg aat tca caa cag gct gat ata Ala Gly Glu Ile Leu Thr Ala Gly Leu Asn Ser Gln Gln Ala Asp Ile 1885 1890 1895	26590
tta cac gct ttt ttg gac gaa tct cgc agt gcc gca tta agc acc tac Leu His Ala Phe Leu Asp Glu Ser Arg Ser Ala Ala Leu Ser Thr Tyr 1900 1905 1910	26638
tat atc cgt caa gtc gcc aag cca gcg gca gcc ata aaa agc cgt gat Tyr Ile Arg Gln Val Ala Lys Pro Ala Ala Ala Ile Lys Ser Arg Asp 1915 1920 1925	26686
gac ttg tac caa tac tta cta att gat aat cag gtt tcc gct gca atc Asp Leu Tyr Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile 1930 1935 1940	26734
aaa act acc cgg att gcc gaa gcc att gcc agc att caa ctg tac gtc Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val 1945 1950 1955 1960	26782
aac cgc acg ctg gaa aat gta gaa gaa aat gcc cat tca ggg gtt atc Asn Arg Thr Leu Glu Asn Val Glu Glu Asn Ala His Ser Gly Val Ile 1965 1970 1975	26830
agc cgt cag ttc ttt atc gac tgg gac aaa tat aac aaa cgc tac agc Ser Arg Gln Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser 1980 1985 1990	26878
acc tgg gcg ggt gtt tct caa tta gtt tac tac ccg gaa aac tat att	26926

Thr Trp Ala Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile	
1995 2000 2005	
gat ccc acc atg cgt atc gga caa acc aaa atg atg gac gca tta ttg	26974
Asp Pro Thr Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu	
2010 2015 2020	
caa tcc gtc agc caa agc caa tta aat gcc gat act gtc gaa gac gcc	27022
Gln Ser Val Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala	
2025 2030 2035 2040	
ttt atg tct tat ctg aca tgc ttt gag caa gtg gct aat ctt aaa gtt	27070
Phe Met Ser Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val	
2045 2050 2055	
att agc gcg tat cac gat aat att aac aac gat caa ggg ctg acc tat	27118
Ile Ser Ala Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr	
2060 2065 2070	
ttt atc gcc ctc agt gaa act gat acc ggt gaa tac tat tgg cgc agt	27166
Phe Ile Gly Leu Ser Glu Thr Asp Thr Gly Glu Tyr Tyr Trp Arg Ser	
2075 2080 2085	
gtc gat cac agt aaa ttc agc gac ggt aaa ttc gcc gct aat gcc tgg	27214
Val Asp His Ser Lys Phe Ser Asp Gly Lys Phe Ala Ala Asn Ala Trp	
2090 2095 2100	
agt gaa tgg cac aaa att gat tgt cca att aat cct tac cga agc act	27262
Ser Glu Trp His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Arg Ser Thr	
2105 2110 2115 2120	
atc cgt cct gtg atg tac aaa tcc cgc ttg tat ctg ctc tgg ttg gaa	27310
Ile Arg Pro Val Met Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu	
2125 2130 2135	
caa aag gag atc act aaa caa aca gga aat agc aaa gat ggc tat caa	27358
Gln Lys Glu Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln	
2140 2145 2150	
acc gag aca gat tat cgt tat gag cta aaa ttg gcg cat atc cgt tat	27406
Thr Glu Thr Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr	
2155 2160 2165	
gac ggt acc tgg aat acg cca atc act ttt gat gtc aat gaa aaa ata	27454
Asp Gly Thr Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Glu Lys Ile	
2170 2175 2180	
tcc aag cta gaa ctg gca aaa aat aaa gcg cct ggg ctc tat tgt gct	27502
Ser Lys Leu Glu Leu Ala Lys Asn Lys Ala Pro Gly Leu Tyr Cys Ala	
2185 2190 2195 2200	
ggt tat caa ggt gaa gat acg ttg ctg gtt atg ttt tat aac caa caa	27550
Gly Tyr Gln Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln	
2205 2210 2215	
gat aca ctc gat agt tat aaa acc gct tca atg caa ggg cta tat atc	27598
Asp Thr Leu Asp Ser Tyr Lys Thr Ala Ser Met Gln Gly Leu Tyr Ile	
2220 2225 2230	
ttt gcc gat atg gaa tat aaa gat atg acc gat gga caa tac aaa tct	27646
Phe Ala Asp Met Glu Tyr Lys Asp Met Thr Asp Gly Gln Tyr Lys Ser	
2235 2240 2245	
tat cgg gac aac agc tat aaa caa ttc gat act aat agt gtc aga aga	27694
Tyr Arg Asp Asn Ser Tyr Lys Gln Phe Asp Thr Asn Ser Val Arg Arg	

2250	2255	2260	
gtg aat aac cgc tat gca gag gat tat gaa att ccc tca tcg gta aat			27742
Val Asn Asn Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Asn			
2265	2270	2275	2280
agc cgt aaa ggc tat gat tgg gga gat tat tat ctc agt atg gta tat			27790
Ser Arg Lys Gly Tyr Asp Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr			
	2285	2290	2295
aac gga gat att cca act att agt tac aaa gcc aca tca agt gat tta			27838
Asn Gly Asp Ile Pro Thr Ile Ser Tyr Lys Ala Thr Ser Ser Asp Leu			
	2300	2305	2310
aaa atc tat atc tcg cca aaa tta aga att att cat aat gga tat gaa			27886
Lys Ile Tyr Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu			
	2315	2320	2325
ggg cag caa cgc aat caa tgc aat cta atg aat aaa tat ggc aaa cta			27934
Gly Gln Gln Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu			
	2330	2335	2340
ggt gat aaa ttt att gtt tat act agc ttg gga gtt aat cca aat aat			27982
Gly Asp Lys Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn			
	2345	2350	2355
tcg tca aat aag ctg atg ttt tac ccc gtt tat caa tat aac gga aat			28030
Ser Ser Asn Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Asn Gly Asn			
	2365	2370	2375
gtc agt ggg ctt agt caa ggg aga tta cta ttc cac cgt gac acc aat			28078
Val Ser Gly Leu Ser Gln Gly Arg Leu Leu Phe His Arg Asp Thr Asn			
	2380	2385	2390
tat tca tct aaa gta gaa gct tgg att cct gga gca gga cgt tct cta			28126
Tyr Ser Ser Lys Val Glu Ala Trp Ile Pro Gly Ala Gly Arg Ser Leu			
	2395	2400	2405
acc aat ccg aat gct gcc att ggt gat gat tat gct aca gac tcg tta			28174
Thr Asn Pro Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu			
	2410	2415	2420
aac aaa ccg aat gat ctt aag caa tac gtc tat atg act gac agt aaa			28222
Asn Lys Pro Asn Asp Leu Lys Gln Tyr Val Tyr Met Thr Asp Ser Lys			
	2425	2430	2435
ggt act gct acc gat gtc tca gga cca gta gat atc aat act gca att			28270
Gly Thr Ala Thr Asp Val Ser Gly Pro Val Asp Ile Asn Thr Ala Ile			
	2445	2450	2455
tcc ccg gca aaa gtt cag gta aca gta aaa gcc ggt agc aaa gaa caa			28318
Ser Pro Ala Lys Val Gln Val Thr Val Lys Ala Gly Ser Lys Glu Gln			
	2460	2465	2470
acg ttt acc gcg gat aaa aat gtc tcc att cag cca tcc cct agc ttt			28366
Thr Phe Thr Ala Asp Lys Asn Val Ser Ile Gln Pro Ser Pro Ser Phe			
	2475	2480	2485
gat gaa atg aat tat caa ttt aat gct ctc gaa ata gat ggc tca agt			28414
Asp Glu Met Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Ser			
	2490	2495	2500
ctg aat ttt act aac aat tca gcc agt att gat att acc ttt acc gca			28462
Leu Asn Phe Thr Asn Asn Ser Ala Ser Ile Asp Ile Thr Phe Thr Ala			
	2505	2510	2515
			2520

ttt gca gag gat gga cgt aaa ctg ggt tat gaa agt ttc agt att cct Phe Ala Glu Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro 2525 2530 2535	28510
att acc cgc aag gtg agt act gat aat tcc ctg acc ctg cgc cat aat Ile Thr Arg Lys Val Ser Thr Asp Asn Ser Leu Thr Leu Arg His Asn 2540 2545 2550	28558
gaa aat ggt gcg caa tat atg caa tgg gga gtc tat cgc att cgt ctt Glu Asn Gly Ala Gln Tyr Met Gln Trp Gly Val Tyr Arg Ile Arg Leu 2555 2560 2565	28606
aat act tta ttt gct cgc caa tta gtt gcg cga gcc act acc ggt att Asn Thr Leu Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile 2570 2575 2580	28654
gat acg att ctg agt atg gaa act cag aat att cag gaa cca cag tta Asp Thr Ile Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu 2585 2590 2595 2600	28702
ggc aaa ggt ttc tac gct acg ttc gtg ata cct ccg tat aac cca tca Gly Lys Gly Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Pro Ser 2605 2610 2615	28750
act cat ggt gat gaa cgt tgg ttt aag ctt tat atc aaa cat gtt gtt Thr His Gly Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val 2620 2625 2630	28798
gat aat aat tca cat att atc tat tca ggt cag cta aaa gat aca aat Asp Asn Asn Ser His Ile Ile Tyr Ser Gly Gln Leu Lys Asp Thr Asn 2635 2640 2645	28846
ata agc acc acg tta ttt atc cct ctt gat gat gtt cca ttg aac caa Ile Ser Thr Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln 2650 2655 2660	28894
gat tac agc gcc aag gtt tac atg acc ttc aag aaa tca cca tca gat Asp Tyr Ser Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp 2665 2670 2675 2680	28942
ggt acc tgg tgg ggc cct cac ttt gtt aga gat gat aaa gga ata gta Gly Thr Trp Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val 2685 2690 2695	28990
aca ata aac cct aaa tcc att ttg acc cac ttt gag agc gtc aat gtc Thr Ile Asn Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val 2700 2705 2710	29038
ctg aat aat att agt agc gaa cca atg gat ttc agc ggc gct aac agc Leu Asn Asn Ile Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser 2715 2720 2725	29086
ctc tat ttt tgg gaa ctg ttc tac tat acc ccg atg ctg gtt gcc caa Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln 2730 2735 2740	29134
cgt ttg ttg cat gag caa aac ttt gat gaa gcg aac cgc tgg ctg aaa Arg Leu Leu His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys 2745 2750 2755 2760	29182
tat gtc tgg agc cca tcc ggg tat att gtt cac ggc cag att cag aat Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn 2765 2770 2775	29230

tat caa tgg aac gtc cgc ccg tta ttg gaa gat acc agt tgg aac agt	29278
Tyr Gln Trp Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser	
2780 2785 2790	
gat cct ttg gat tcc gtc gat cct gac gcg gta gcg cag cac gat ccg	29326
Asp Pro Leu Asp Ser Val Asp Pro Asp Ala Val Ala Gln His Asp Pro	
2795 2800 2805	
atg cac tat aaa gtt tca acc ttt atg cgc acc ctt gat ctg ttg atc	29374
Met His Tyr Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile	
2810 2815 2820	
gcg cgc gcc gac cat gct tac cgc caa ttg gag cgc gat acg ctt aac	29422
Ala Arg Gly Asp His Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Asn	
2825 2830 2835 2840	
gaa gcg aag atg tgg tat atg caa gcg ctg cat ctg tta gcc gat aaa	29470
Glu Ala Lys Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys	
2845 2850 2855	
cct tat ctg ccg ctg agt acc aca tgg aat gat cca cga ctg gac aaa	29518
Pro Tyr Leu Pro Leu Ser Thr Thr Trp Asn Asp Pro Arg Leu Asp Lys	
2860 2865 2870	
gcc gcg gat att act acc caa agt gct cat tcc agc tca ata gtc gct	29566
Ala Ala Asp Ile Thr Thr Gln Ser Ala His Ser Ser Ser Ile Val Ala	
2875 2880 2885	
ttg cgg cag agt aca ccg gcg ctt tta tca ttg cgc agc gcc aat acc	29614
Leu Arg Gln Ser Thr Pro Ala Leu Leu Ser Leu Arg Ser Ala Asn Thr	
2890 2895 2900	
ctg acc gat ctc ttc ctg ccg caa atc aat gaa gtg atg atg aat tac	29662
Leu Thr Asp Leu Phe Leu Pro Gln Ile Asn Glu Val Met Met Asn Tyr	
2905 2910 2915 2920	
tgg caa aca tta gct cag aga gta tac aac ctg cgc cac aac ctc tct	29710
Trp Gln Thr Leu Ala Gln Arg Val Tyr Asn Leu Arg His Asn Leu Ser	
2925 2930 2935	
atc gac ggt cag ccg tta tat ctg cca atc tat gcc aca ccg gcg gac	29758
Ile Asp Gly Gln Pro Leu Tyr Leu Pro Ile Tyr Ala Thr Pro Ala Asp	
2940 2945 2950	
ccg aaa gcg tta ctc agc gcc gct gtt gcc act tct caa ggt gga gcc	29806
Pro Lys Ala Leu Leu Ser Ala Ala Val Ala Thr Ser Gln Gly Gly Gly	
2955 2960 2965	
aag ctg ccg gag tca ttt atg tcc ctg tgg cgt ttc ccg cac atg ctg	29854
Lys Leu Pro Glu Ser Phe Met Ser Leu Trp Arg Phe Pro His Met Leu	
2970 2975 2980	
gaa aat gct cgc agc atg gtt agc cag ctc acc caa ttc gcc tcc acg	29902
Glu Asn Ala Arg Ser Met Val Ser Gln Leu Thr Gln Phe Gly Ser Thr	
2985 2990 2995 3000	
tta caa aat att atc gaa cgt cag gac gca gaa gcg ctc aat gcg tta	29950
Leu Gln Asn Ile Ile Glu Arg Gln Asp Ala Glu Ala Leu Asn Ala Leu	
3005 3010 3015	
tta caa aat cag gcc gca gag ctg ata ttg act aac ctg agt att caa	29998
Leu Gln Asn Gln Ala Ala Glu Leu Ile Leu Thr Asn Leu Ser Ile Gln	
3020 3025 3030	
gac aaa acc att gaa gaa ctg gat gcc gag aaa acc gtg ctg gaa aaa	30046

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Asp Lys Thr Ile Glu Glu Leu Asp Ala Glu Lys Thr Val Leu Glu Lys	
3035 3040 3045	
tcc aaa gcg gga gca caa tcg cgc ttt gat agc tat agc aaa ctg cat	30094
Ser Lys Ala Gly Ala Gln Ser Arg Phe Asp Ser Tyr Ser Lys Leu His	
3050 3055 3060	
gat gaa aac atc aac gcc ggt gaa aac caa gct atg acg cta cga gcg	30142
Asp Glu Asn Ile Asn Ala Gly Glu Asn Gln Ala Met Thr Leu Arg Ala	
3065 3070 3075 3080	
tcc gca gcc ggg ctt acc acg gcg gtt cag gca tcc cgt ctg gcc ggc	30190
Ser Ala Ala Gly Leu Thr Thr Ala Val Gln Ala Ser Arg Leu Ala Gly	
3085 3090 3095	
gca gcg gct gat ctg gtg cct aac atc ttc ggc ttc gcc ggt ggt ggt	30238
Ala Ala Ala Asp Leu Val Pro Asn Ile Phe Gly Phe Ala Gly Gly Gly	
3100 3105 3110	
agc cgt tgg ggg gct atc gct gag gcg acc ggc tat gta atg gaa ttt	30286
Ser Arg Trp Gly Ala Ile Ala Glu Ala Thr Gly Tyr Val Met Glu Phe	
3115 3120 3125	
tcc gct aat gtt atg aat acc gaa gcg gat aaa att agc caa tct gaa	30334
Ser Ala Asn Val Met Asn Thr Glu Ala Asp Lys Ile Ser Gln Ser Glu	
3130 3135 3140	
acc tac cgt cgt cgc cgt cag gag tgg gaa att cag cgt aat aat gcc	30382
Thr Tyr Arg Arg Arg Arg Gln Glu Trp Glu Ile Gln Arg Asn Asn Ala	
3145 3150 3155 3160	
gaa gcg gag ctg aaa caa ctc gat gcc caa ctt aaa tcg ctg gca gta	30430
Glu Ala Glu Leu Lys Gln Leu Asp Ala Gln Leu Lys Ser Leu Ala Val	
3165 3170 3175	
cgc cgt gaa gcc gcc gta ttg caa aaa acc agc ctg aaa acc caa caa	30478
Arg Arg Glu Ala Ala Val Leu Gln Lys Thr Ser Leu Lys Thr Gln Gln	
3180 3185 3190	
gag cag acc caa gcc caa ttg gcc ttc ctg caa cgt aag ttc agc aat	30526
Glu Gln Thr Gln Ala Gln Leu Ala Phe Leu Gln Arg Lys Phe Ser Asn	
3195 3200 3205	
caa gcg ttg tac aac tgg cta cgt ggc cga ctg gca gca att tac ttc	30574
Gln Ala Leu Tyr Asn Trp Leu Arg Gly Arg Leu Ala Ala Ile Tyr Phe	
3210 3215 3220	
caa ttc tac gac ttg gct atc gcg cgt tgt tta atg gca gag cag gct	30622
Gln Phe Tyr Asp Leu Ala Ile Ala Arg Cys Leu Met Ala Glu Gln Ala	
3225 3230 3235 3240	
tac cgt tgg gaa att agc gat gac tct gct cgc ttt att aaa ccg ggc	30670
Tyr Arg Trp Glu Ile Ser Asp Asp Ser Ala Arg Phe Ile Lys Pro Gly	
3245 3250 3255	
gcc tgg caa gga acc tat gca ggt ctg ctg gca ggt gaa acc ttg atg	30718
Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu Ala Gly Glu Thr Leu Met	
3260 3265 3270	
cta agt ttg gca caa atg gaa gac gcc cat tta aga cgc gat aaa cgc	30766
Leu Ser Leu Ala Gln Met Glu Asp Ala His Leu Arg Arg Asp Lys Arg	
3275 3280 3285	
gca tta gag gtc gaa cgt aca gta tcg ctg gcc gaa att tat gct ggt	30814
Ala Leu Glu Val Glu Arg Thr Val Ser Leu Ala Glu Ile Tyr Ala Gly	

3290	3295	3300	
tta ccg caa gat aaa ggc cca ttc tcc ctg acg	caa gaa atc gag aag	30862	
Leu Pro Gln Asp Lys Gly Pro Phe Ser Leu Thr	Gln Glu Ile Glu Lys		
3305	3310 3315 3320		
ctg gtg aat gca ggt tca ggc agc gcc ggc agt ggt aat aat aat ttg	30910		
Leu Val Asn Ala Gly Ser Gly Ser Ala Gly Ser Gly Asn Asn Asn Leu			
3325	3330 3335		
gca ttt ggc gcc ggc acg gac act aaa act tct ttg cag gca tcc att	30958		
Ala Phe Gly Ala Gly Thr Asp Thr Lys Thr Ser Leu Gln Ala Ser Ile			
3340	3345 3350		
tca tta gct gat tta aaa att cgt gag gat tac ccg gaa tct att ggc	31006		
Ser Leu Ala Asp Leu Lys Ile Arg Glu Asp Tyr Pro Glu Ser Ile Gly			
3355	3360 3365		
aaa atc cga cgc atc aaa cag atc agc gtt acc ctg ccg gcg cta ttg	31054		
Lys Ile Arg Arg Ile Lys Gln Ile Ser Val Thr Leu Pro Ala Leu Leu			
3370	3375 3380		
gga cct tat cag gat gtg cag gca ata tta tct tac ggc gat aaa gcc	31102		
Gly Pro Tyr Gln Asp Val Gln Ala Ile Leu Ser Tyr Gly Asp Lys Ala			
3385	3390 3395 3400		
gga tta gcg aac ggc tgt gca gcg ctg gcc gtt tcc cac ggt acg aat	31150		
Gly Leu Ala Asn Gly Cys Ala Ala Leu Ala Val Ser His Gly Thr Asn			
3405	3410 3415		
gac agc ggt caa ttc cag ctc gat ttc aac gat ggc aaa ttc ctg ccg	31198		
Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys Phe Leu Pro			
3420	3425 3430		
ttt gaa ggt atc gcc att gat caa ggt acg cta aca ctg agt ttt cct	31246		
Phe Glu Gly Ile Ala Ile Asp Gln Gly Thr Leu Thr Leu Ser Phe Pro			
3435	3440 3445		
aat gca tca acg cca gcc aaa ggt aaa caa gcc act atg tta aaa acc	31294		
Asn Ala Ser Thr Pro Ala Lys Gly Lys Gln Ala Thr Met Leu Lys Thr			
3450	3455 3460		
ctg aac gat atc att ttg cat att cgc tac acc att aag taa	31336		
Leu Asn Asp Ile Ile Leu His Ile Arg Tyr Thr Ile Lys			
3465	3470 3475		
ccatcccaac acagaactaa gacaggcccc gaatcggggt ctggtaagga gtttct atg	31395		
	Met		
cag aat tca cag aca ttc agc atg acc gag ctg tca tta cct aag ggc	31443		
Gln Asn Ser Gln Thr Phe Ser Met Thr Glu Leu Ser Leu Pro Lys Gly			
3480	3485 3490 3495		
ggc ggc gcc att acc ggt atg ggt gaa gca tta acg ccg gcc ggg ccg	31491		
Gly Gly Ala Ile Thr Gly Met Gly Glu Ala Leu Thr Pro Ala Gly Pro			
3500	3505 3510		
gat ggt atg gca gcc tta tcg ctg cca ttg ccc att tct gcc gga cgt	31539		
Asp Gly Met Ala Ala Leu Ser Leu Pro Leu Pro Ile Ser Ala Gly Arg			
3515	3520 3525		
ggt tat gcc ccc tcg ctc acg ctg aac tac aac agc gga acc ggt aac	31587		
Gly Tyr Ala Pro Ser Leu Thr Leu Asn Tyr Asn Ser Gly Thr Gly Asn			
3530	3535 3540		

agc cgc ttc ggt ctc ggt tgg gac tgt aac gtc atg aca att cgt cgt 31635
 Ser Pro Phe Gly Leu Gly Trp Asp Cys Asn Val Met Thr Ile Arg Arg
 3545 3550 3555

cgc acc agt acc ggc gtg cgc aat tat gat gaa acc gat act ttt ctg 31683
 Arg Thr Ser Thr Gly Val Pro Asn Tyr Asp Glu Thr Asp Thr Phe Leu
 3560 3565 3570 3575

ggg cgc gaa ggt gaa gtg ttg gtc gta gca tta aat gag gca ggt caa 31731
 Gly Pro Glu Gly Glu Val Leu Val Val Ala Leu Asn Glu Ala Gly Gln
 3580 3585 3590

gct gat atc cgc agt gaa tcc tca tta cag ggc atc aat ttg ggg atg 31779
 Ala Asp Ile Arg Ser Glu Ser Ser Leu Gln Gly Ile Asn Leu Gly Met
 3595 3600 3605

acc ttc acc gtt acc ggt tat cgc tcc cgt ttg gaa agc cac ttt agc 31827
 Thr Phe Thr Val Thr Gly Tyr Arg Ser Arg Leu Glu Ser His Phe Ser
 3610 3615 3620

cgg ttg gaa tac tgg caa ccc caa aca aca ggc gca acc gat ttc tgg 31875
 Arg Leu Glu Tyr Trp Gln Pro Gln Thr Thr Gly Ala Thr Asp Phe Trp
 3625 3630 3635

ctg ata tac agc ccc gac gga caa gcc cat tta ctg ggc aaa aat cct 31923
 Leu Ile Tyr Ser Pro Asp Gly Gln Ala His Leu Leu Gly Lys Asn Pro
 3640 3645 3650 3655

caa gca cgc atc agc aat cca cta aat gtt aac caa aca ggc caa tgg 31971
 Gln Ala Arg Ile Ser Asn Pro Leu Asn Val Asn Gln Thr Ala Gln Trp
 3660 3665 3670

cta ttg gaa gcc tcg gta tca tcc cac ggc gag cag att tat tat cag 32019
 Leu Leu Glu Ala Ser Val Ser Ser His Gly Glu Gln Ile Tyr Tyr Gln
 3675 3680 3685

tat cga gcc gaa gat gaa act gat tgc gaa act gac gaa ctc aca gcc 32067
 Tyr Arg Ala Glu Asp Glu Thr Asp Cys Glu Thr Asp Glu Leu Thr Ala
 3690 3695 3700

cac cgc aac aca acc gtc cag cgc tac ctg caa gta gta cat tac ggt 32115
 His Pro Asn Thr Thr Val Gln Arg Tyr Leu Gln Val Val His Tyr Gly
 3705 3710 3715

aat cta acc gcc agc gaa gta ttt ccc acg cta aat gga gat gat cca 32163
 Asn Leu Thr Ala Ser Glu Val Phe Pro Thr Leu Asn Gly Asp Asp Pro
 3720 3725 3730 3735

ctc aaa tct ggc tgg ttg ttc tgt tta gta ttt gat tac ggt gag cgc 32211
 Leu Lys Ser Gly Trp Leu Phe Cys Leu Val Phe Asp Tyr Gly Glu Arg
 3740 3745 3750

aaa aac agc tta tct gaa atg cgc cca ttt aaa gcc aca agt aac tgg 32259
 Lys Asn Ser Leu Ser Glu Met Pro Pro Phe Lys Ala Thr Ser Asn Trp
 3755 3760 3765

ctt tgc cgc aaa gac cgt ttt tcc cgt tat gaa tac ggt ttt gca ttg 32307
 Leu Cys Arg Lys Asp Arg Phe Ser Arg Tyr Glu Tyr Gly Phe Ala Leu
 3770 3775 3780

cgc acc cgg cgc tta tgt cgc caa ata ctg atg ttt cac cgt ctg caa 32355
 Arg Thr Arg Arg Leu Cys Arg Gln Ile Leu Met Phe His Arg Leu Gln
 3785 3790 3795

acc ctg tct ggt cag gca aaa ggc gac gat gaa ccc gca tta gtt tca 32403

Thr 3800	Leu	Ser	Gly	Gln	Ala	Lys	Gly	Asp	Asp	Glu	Pro	Ala	Leu	Val	Ser		
3805																3810	3815
cgt	ctg	ata	ctg	gat	tat	gac	gaa	aac	gcg	gtg	gtc	agt	acg	ctc	gtt	32451	
Arg	Leu	Ile	Leu	Asp	Tyr	Asp	Glu	Asn	Ala	Val	Val	Ser	Thr	Leu	Val		
3820																3825	3830
tct	gtc	cgc	cga	gtg	gga	cat	gag	caa	gat	ggc	aca	acg	gcg	gtc	gcc	32499	
Ser	Val	Arg	Arg	Val	Gly	His	Glu	Gln	Asp	Gly	Thr	Thr	Ala	Val	Ala		
3835																3840	3845
ctg	ccg	cca	ttg	gaa	ctg	gct	tat	cag	cct	ttt	gaa	cca	gaa	caa	aaa	32547	
Leu	Pro	Pro	Leu	Glu	Leu	Ala	Tyr	Gln	Pro	Phe	Glu	Pro	Glu	Gln	Lys		
3850																3855	3860
gca	ctc	tgg	cga	cca	atg	gat	gta	ctg	gcg	aat	ttc	aac	acc	atc	caa	32595	
Ala	Leu	Trp	Arg	Pro	Met	Asp	Val	Leu	Ala	Asn	Phe	Asn	Thr	Ile	Gln		
3865																3870	3875
cgc	tgg	caa	ctg	ctt	gat	ctg	caa	ggc	gaa	ggc	gta	ccc	ggg	att	ctg	32643	
Arg	Trp	Gln	Leu	Leu	Asp	Leu	Gln	Gly	Glu	Gly	Val	Pro	Gly	Ile	Leu		
3880																3885	3890
tat	cag	gat	aaa	aat	ggc	tgg	tgg	tat	cga	tct	gct	caa	cgt	cag	aca	32691	
Tyr	Gln	Asp	Lys	Asn	Gly	Trp	Trp	Tyr	Arg	Ser	Ala	Gln	Arg	Gln	Thr		
3900																3905	3910
ggg	gaa	gag	atg	aat	gcg	gtc	acc	tgg	ggc	aaa	atg	caa	ctc	ctt	cct	32739	
Gly	Glu	Glu	Met	Asn	Ala	Val	Thr	Trp	Gly	Lys	Met	Gln	Leu	Leu	Pro		
3915																3920	3925
atc	acg	ccc	gct	att	cag	gat	aac	gcc	tca	ctg	atg	gat	att	aat	ggg	32787	
Ile	Thr	Pro	Ala	Ile	Gln	Asp	Asn	Ala	Ser	Leu	Met	Asp	Ile	Asn	Gly		
3930																3935	3940
gat	ggg	caa	ctg	gat	tgg	gtt	atc	acc	ggg	ccg	ggg	cta	agg	ggg	tat	32835	
Asp	Gly	Gln	Leu	Asp	Trp	Val	Ile	Thr	Gly	Pro	Gly	Leu	Arg	Gly	Tyr		
3945																3950	3955
cac	agc	cag	cat	cca	gat	ggc	agt	tgg	aca	cgt	ttt	acg	ccg	ttg	cac	32883	
His	Ser	Gln	His	Pro	Asp	Gly	Ser	Trp	Thr	Arg	Phe	Thr	Pro	Leu	His		
3960																3965	3970
gcc	tta	ccg	ata	gaa	tat	acc	cat	ccc	cgc	gcc	caa	ctt	gcg	gat	tta	32931	
Ala	Leu	Pro	Ile	Glu	Tyr	Thr	His	Pro	Arg	Ala	Gln	Leu	Ala	Asp	Leu		
3980																3985	3990
atg	ggg	gcc	ggg	ctg	tcc	gat	tta	gtg	ctg	att	ggg	ccc	aaa	agc	gtg	32979	
Met	Gly	Ala	Gly	Leu	Ser	Asp	Leu	Val	Leu	Ile	Gly	Pro	Lys	Ser	Val		
3995																4000	4005
cgt	ttg	tat	gcc	aat	aac	cgt	gat	ggg	ttt	acc	gaa	gga	cgg	gat	gtg	33027	
Arg	Leu	Tyr	Ala	Asn	Asn	Arg	Asp	Gly	Phe	Thr	Glu	Gly	Arg	Asp	Val		
4010																4015	4020
gtg	caa	tcc	ggg	ggg	atc	acc	ctg	ccg	tta	ccg	ggc	gcc	gat	gcg	cgt	33075	
Val	Gln	Ser	Gly	Gly	Ile	Thr	Leu	Pro	Leu	Pro	Gly	Ala	Asp	Ala	Arg		
4025																4030	4035
aag	tta	gtg	gcc	ttt	agc	gac	gta	ctc	ggg	tca	ggc	caa	gca	cat	ttg	33123	
Lys	Leu	Val	Ala	Phe	Ser	Asp	Val	Leu	Gly	Ser	Gly	Gln	Ala	His	Leu		
4040																4045	4050
gtt	g																

4060	4065	4070	
ggc cgt ttt ggt cag cca atc aca ttg ccg gga ttt agc caa tcc gcc Gly Arg Phe Gly Gln Pro Ile Thr Leu Pro Gly Phe Ser Gln Ser Ala 4075 4080 4085			33219
gcc aat ttt aat cct gat cga gtt cat ctg gcc gat ctg gac ggt agt Ala Asn Phe Asn Pro Asp Arg Val His Leu Ala Asp Leu Asp Gly Ser 4090 4095 4100			33267
ggt cct gcc gat ctg att tat gtt cat gct gac cat ctg gat att ttc Gly Pro Ala Asp Leu Ile Tyr Val His Ala Asp His Leu Asp Ile Phe 4105 4110 4115			33315
agc aat gaa agt ggt aac ggt ttt gca caa cca ttc aca ctc cgt ttt Ser Asn Glu Ser Gly Asn Gly Phe Ala Gln Pro Phe Thr Leu Arg Phe 4120 4125 4130 4135			33363
cct gac gcc ctg cgt ttt gat gat act tgc cag cta caa gtg gct gat Pro Asp Gly Leu Arg Phe Asp Asp Thr Cys Gln Leu Gln Val Ala Asp 4140 4145 4150			33411
gta cag gga tta ggg gtt gtc agc ctg atc ctg agc gta ccg cat atg Val Gln Gly Leu Gly Val Val Ser Leu Ile Leu Ser Val Pro His Met 4155 4160 4165			33459
gcg cca cac cat tgg cgc tgc gat ctg acc aac gcg aaa ccg tgg tta Ala Pro His His Trp Arg Cys Asp Leu Thr Asn Ala Lys Pro Trp Leu 4170 4175 4180			33507
ctc agt gaa atg aac aac aac atg gga gcc cat cac acc ctg cat tac Leu Ser Glu Met Asn Asn Asn Met Gly Ala His His Thr Leu His Tyr 4185 4190 4195			33555
cgt agc tcc gtc cag ttt tgg ctg gat gaa aaa gcc gca gcc tta gct Arg Ser Ser Val Gln Phe Trp Leu Asp Glu Lys Ala Ala Ala Leu Ala 4200 4205 4210 4215			33603
acc gga caa aca ccg gtc tgt tac ctg ccc ttc ccg gtc cat acc ctg Thr Gly Gln Thr Pro Val Cys Tyr Leu Pro Phe Pro Val His Thr Leu 4220 4225 4230			33651
tgg caa aca gaa acc gag gat gaa atc agc gcc aat aaa tta gtg acc Trp Gln Thr Glu Thr Glu Asp Glu Ile Ser Gly Asn Lys Leu Val Thr 4235 4240 4245			33699
act tta cgt tac gct cac gcc gcc tgg gat gga cgt gag ccg gaa ttt Thr Leu Arg Tyr Ala His Gly Ala Trp Asp Gly Arg Glu Arg Glu Phe 4250 4255 4260			33747
cgc gcc ttt gcc tat gtt gag cag aca gac agc cat caa ctg gct caa Arg Gly Phe Gly Tyr Val Glu Gln Thr Asp Ser His Gln Leu Ala Gln 4265 4270 4275			33795
ggc aat gcg ccg gaa cgt aca tca ccg gca ctt acc aaa aac tgg tat Gly Asn Ala Pro Glu Arg Thr Ser Pro Ala Leu Thr Lys Asn Trp Tyr 4280 4285 4290 4295			33843
gcc acc gga atc cct gag gta gac aat acg cta tct gcc ggg tat tgg Ala Thr Gly Ile Pro Glu Val Asp Asn Thr Leu Ser Ala Gly Tyr Trp 4300 4305 4310			33891
cgc ggt gat acg cag gct ttc act ggt ttt acg cca cac ttt act ctc Arg Gly Asp Thr Gln Ala Phe Thr Gly Phe Thr Pro His Phe Thr Leu 4315 4320 4325			33939

tgg aaa gag ggc aaa gat gtt cca ctg aca ccg gaa gat gac cac aat Trp Lys Glu Gly Lys Asp Val Pro Leu Thr Pro Glu Asp Asp His Asn 4330 4335 4340	33987
ctg tac tgg tta aac cgg gca cta aaa ggt caa cca ctg cgt agt gaa Leu Tyr Trp Leu Asn Arg Ala Leu Lys Gly Gln Pro Leu Arg Ser Glu 4345 4350 4355	34035
ctc tac ggg cta gat ggc agc gca cag cag aag atc ccc tat aca gtg Leu Tyr Gly Leu Asp Gly Ser Ala Gln Gln Lys Ile Pro Tyr Thr Val 4360 4365 4370 4375	34083
act gaa tcc cgc cca caa gtg cgc caa tta caa gat aac act acc ctt Thr Glu Ser Arg Pro Gln Val Arg Gln Leu Gln Asp Asn Thr Thr Leu 4380 4385 4390	34131
tcc ccg gtg ctc tgg gcc tca gtg gtg gaa agt cgt agt tat cac tat Ser Pro Val Leu Trp Ala Ser Val Glu Ser Arg Ser Tyr His Tyr 4395 4400 4405	34179
gaa cgt atc atc agc gat ccc caa tgc aat cag gat atc act ctg tcc Glu Arg Ile Ile Ser Asp Pro Gln Cys Asn Gln Asp Ile Thr Leu Ser 4410 4415 4420	34227
agt gac cta ttc ggg caa ccg ctg aaa cag gtt tca gtg caa tat ccc Ser Asp Leu Phe Gly Gln Pro Leu Lys Gln Val Ser Val Gln Tyr Pro 4425 4430 4435	34275
cgc cgc aat aaa cca aca acc aat ccg tat ccc gat aca cta cca gat Arg Arg Asn Lys Pro Thr Thr Asn Pro Tyr Pro Asp Thr Leu Pro Asp 4440 4445 4450 4455	34323
act ctg ttt gcc agc agt tat gac gac caa caa caa cta ttg cgg tta Thr Leu Phe Ala Ser Ser Tyr Asp Asp Gln Gln Gln Leu Leu Arg Leu 4460 4465 4470	34371
acc tac cag caa tcc agt tgg cat cat cta att gct aat gaa ctc aga Thr Tyr Gln Gln Ser Ser Trp His His Leu Ile Ala Asn Glu Leu Arg 4475 4480 4485	34419
gtg tta gga tta ccg gat ggt aca cgc agt gat gct ttc act tac gat Val Leu Gly Leu Pro Asp Gly Thr Arg Ser Asp Ala Phe Thr Tyr Asp 4490 4495 4500	34467
gct aaa cac gtg cct gtt gat ggt tta aat ctg gaa gct cta tgt gct Ala Lys His Val Pro Val Asp Gly Leu Asn Leu Glu Ala Leu Cys Ala 4505 4510 4515	34515
gaa aat agc ctg att gcc gat gat aaa cct cgc gaa tac ctc aac cag Glu Asn Ser Leu Ile Ala Asp Asp Lys Pro Arg Glu Tyr Leu Asn Gln 4520 4525 4530 4535	34563
caa cga acg ttc tat acc gat ggg aaa acc gat gga aaa aat cca acg Gln Arg Thr Phe Tyr Thr Asp Gly Lys Thr Asp Gly Lys Asn Pro Thr 4540 4545 4550	34611
cca ctg aaa aca ccg aca cga cag gct tta atc gcc ttt acc gaa acg Pro Leu Lys Thr Pro Thr Arg Gln Ala Leu Ile Ala Phe Thr Glu Thr 4555 4560 4565	34659
gcg gta tta acg gaa tct ctg tta tcc gca ttt gat ggc ggt atc acg Ala Val Leu Thr Glu Ser Leu Leu Ser Ala Phe Asp Gly Gly Ile Thr 4570 4575 4580	34707

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cca gat gaa tta ccc ggc ctt ctg aca caa gca gga tac caa caa gaa Pro Asp Glu Leu Pro Gly Leu Leu Thr Gln Ala Gly Tyr Gln Gln Glu 4585 4590 4595	34755
cct tat ctg ttc cca ctc agt ggc gaa aac caa gtc tgg gta gca cgc Pro Tyr Leu Phe Pro Leu Ser Gly Glu Asn Gln Val Trp Val Ala Arg 4600 4605 4610 4615	34803
aaa ggc tat acc gat tac gga act gag gta caa ttt tgg cgt cct gtc Lys Gly Tyr Thr Asp Tyr Gly Thr Glu Val Gln Phe Trp Arg Pro Val 4620 4625 4630	34851
gca caa cgt aac acc cag tta acc ggg aaa acg act cta aaa tgg gat Ala Gln Arg Asn Thr Gln Leu Thr Gly Lys Thr Thr Leu Lys Trp Asp 4635 4640 4645	34899
acc cac tac tgt gtc atc act caa acc caa gac gcg gct ggt ttg act Thr His Tyr Cys Val Ile Thr Gln Thr Gln Asp Ala Ala Gly Leu Thr 4650 4655 4660	34947
gtc tca gcc aat tat gac tgg cgt ttt ctc aca cct atg caa ctg act Val Ser Ala Asn Tyr Asp Trp Arg Phe Leu Thr Pro Met Gln Leu Thr 4665 4670 4675	34995
gat atc aac gat aat gtg cat atc ata acc ttg gat gcg cta gga cgc Asp Ile Asn Asp Asn Val His Ile Ile Thr Leu Asp Ala Leu Gly Arg 4680 4685 4690 4695	35043
cct gtc act caa cgt ttc tgg gga atc gaa aat ggt gtg gca aca ggt Pro Val Thr Gln Arg Phe Trp Gly Ile Glu Asn Gly Val Ala Thr Gly 4700 4705 4710	35091
tac tct tca cca gaa gca aaa cca ttc act cca cca gtc gat gtc aat Tyr Ser Ser Pro Glu Ala Lys Pro Phe Thr Pro Pro Val Asp Val Asn 4715 4720 4725	35139
gct gcc att gct ctg acc gga cca ctc cct gtc gcg cag tgt ctg gtc Ala Ala Ile Ala Leu Thr Gly Pro Leu Pro Val Ala Gln Cys Leu Val 4730 4735 4740	35187
tat gcg ccg gac agt tgg atg ccg cta ttc ggt cag gaa acc ttc aac Tyr Ala Pro Asp Ser Trp Met Pro Leu Phe Gly Gln Glu Thr Phe Asn 4745 4750 4755	35235
aca tta acg cag gaa gag caa aag aca ctg cgt gat tta cgg att atc Thr Leu Thr Gln Glu Glu Gln Lys Thr Leu Arg Asp Leu Arg Ile Ile 4760 4765 4770 4775	35283
aca gaa gat tgg cgt att tgc gca ctg gct cgc cgc cgt tgg cta caa Thr Glu Asp Trp Arg Ile Cys Ala Leu Ala Arg Arg Arg Trp Leu Gln 4780 4785 4790	35331
agt caa aaa gcc ggc aca cca ttg gtt aag ctg tta acc aac agc atc Ser Gln Lys Ala Gly Thr Pro Leu Val Lys Leu Leu Thr Asn Ser Ile 4795 4800 4805	35379
ggt tta cct ccc cac aac ctc atg ctg gct acg gac cgt tat gac cgt Gly Leu Pro Pro His Asn Leu Met Leu Ala Thr Asp Arg Tyr Asp Arg 4810 4815 4820	35427
gat tct gaa cag caa att cgt caa caa gtc gca ttc agt gat ggt ttt Asp Ser Glu Gln Gln Ile Arg Gln Gln Val Ala Phe Ser Asp Gly Phe 4825 4830 4835	35475
ggc cgt ttg ttg caa gcg gct gtg cgg cat gag gca ggc gaa gcc tgg	35523

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Gly Arg Leu Leu Gln Ala Ala Val Arg His Glu Ala Gly Glu Ala Trp
 4840 4845 4850 4855
 caa cgt aac caa gac ggt tct ctg gtg aca aaa atg gaa gat acc aaa 35571
 Gln Arg Asn Gln Asp Gly Ser Leu Val Thr Lys Met Glu Asp Thr Lys
 4860 4865 4870
 acg cgc tgg gcg att acg gga cgc act gaa tat gac aat aag ggg cag 35619
 Thr Arg Trp Ala Ile Thr Gly Arg Thr Glu Tyr Asp Asn Lys Gly Gln
 4875 4880 4885
 gcg ata cga act tat cag ccc tat ttc ctc aat gac tgg cga tat gtg 35667
 Ala Ile Arg Thr Tyr Gln Pro Tyr Phe Leu Asn Asp Trp Arg Tyr Val
 4890 4895 4900
 agt gat gac agc gcc aga aaa gag gcc tat gcc gat act cat atc tat 35715
 Ser Asp Asp Ser Ala Arg Lys Glu Ala Tyr Ala Asp Thr His Ile Tyr
 4905 4910 4915
 gat ccg att ggg cgg gaa atc caa gtt atc acg gca aaa ggc tgg ctg 35763
 Asp Pro Ile Gly Arg Glu Ile Gln Val Ile Thr Ala Lys Gly Trp Leu
 4920 4925 4930 4935
 cgg cag aac caa tat ttc ccg tgg ttt acc gtg agt gaa gat gaa aat 35811
 Arg Gln Asn Gln Tyr Phe Pro Trp Phe Thr Val Ser Glu Asp Glu Asn
 4940 4945 4950
 gat ttg tcc gct gac gcg ctc gtg taa ttgaatcaag attcgctcgt 35858
 Asp Leu Ser Ala Asp Ala Leu Val
 4955 4960
 ttaatgttaa cgagcgaata taatatacct aatagatttc gagttgcagc gcggcggcaa 35918
 gtgaacgaat cccaggagc atagataact atgtgactgg ggtgagtga agcagccaac 35978
 aaagcagcag cttgaaagat gaagggtata aataagaaac tgcattgtga gttctaaata 36038
 gagtagcagc atattttatt gccttttatt tcataggtaa taaaattcaa ttgctgtaaa 36098
 aatctgtcat catgagaact aaaaataaca actttctctt ctgcaagaga aatcaataat 36158
 tcaattaaaa atgttataga atctgaatca agaccatttg ttggctcatc aaaaatataa 36218
 acatccgcat cggtaataaa agctgatgtc aatagaaatt tcttttttat cccaagtgac 36278
 atatgtccat actcaatacc agaataatta gatataccaa aaccatttaa atagtaatct 36338
 aattgatatt ttaaattact tttcctataa cgctgactta aattaatcac atccattccc 36398
 gtgatgaaat tataaaagtt aacattatcc gatagataaa aaccatgctg ttgcaaatta 36458
 aatcggctct tttctccctt ttttataaaa ttaaccattc cttttttaac cttattttaca 36518
 ccagcaatac ttgaaagaaa agtcgtttta cccgccccat taactccgc aatacggttt 36578
 aatccaaccc gaaaatcaca attgactcct gaaaaaatag tcttaccatt aataacaacc 36638
 tetaacccaa taacttcaag cataaataac ccctaaaaat aacgtaaaaa agaaaataac 36698
 accaacaata ataattttcg tgtattgctg tctcaacaga gaaatagaag aaacaataat 36758
 agaaagaaaa gcataagata aaaatataat cacagaaaaa gatttaacaa caagaaagca 36818
 aaaaataaaa aaacaaagca aataaaaaaa caagaaata ccataattaa aaaagaatat 36878

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 attataaaat aacaacatgc atatatataa aacaacactg gcatatatta atgatatata 36998
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 tatataaggc aatgaaaaaa aacctgatga aaataatttt ttatttctat taattatata 37178
 acatggtgtg aaattcaaata ataatatcaa tgctactaat ggaataacta atgtaaaaat 37238
 caaatcatat aatattccac tcttgaatga tgccgccaga agaaagaaca cagcaacaat 37298
 aaaaaaatgc aaaaaactta attcaaataa gcaaaatcca attacagcaa aagaaactat 37358
 caaaaaaac acagatgaaa ggtaatgcaa ataattaaca ttttcgtaaa aaaacctat 37418
 aaagaagaaa ataactatcg gaaaagcact ataaataaaa aaaacgatac gactaaaaaa 37478
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 ccttatgtta atcaataaaa ataccatata taccattaaa gatatggcag taaaataaaa 37598
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 gataccactg aactttgccg gaagtaataa aagaaaaagg aatataatga catttttatt 37718
 cccagacgca aatttcttta tctacctttt atattccaag gcatcagoga ttattaaatt 37778
 catactgcct ctctaaaacc aaaatctaaa taatgtcctt ggtgaatcct tagggaattt 37838
 cgtcctggaa tgcaaatata aatagttact gaaaacaata cattgatttt taattaaata 37898
 ctggcgatat gaccttaatg atgtactttt atttccagt attcaattcg 37948

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<211> 954

<212> PRT

<213> Photorhabdus luminescens

<400> 12

Met Lys Asn Ile Asp Pro Lys Leu Tyr Gln Lys Thr Pro Val Val Asn
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Ile Tyr Asp Asn Arg Gly Leu Thr Ile Arg Asn Ile Asp Phe His Arg
 20 25 30

Thr Thr Ala Asn Gly Asp Thr Asp Ile Arg Ile Thr Arg His Gln Tyr
 35 40 45

Asp Ser Leu Gly His Leu Ser Gln Ser Thr Asp Pro Arg Leu Tyr Glu
 50 55 60

Ala Lys Gln Lys Ser Asn Phe Leu Trp Gln Tyr Asp Leu Thr Gly Asn
 65 70 75 80

Ile Leu Cys Thr Glu Ser Val Asp Ala Gly Arg Thr Val Thr Leu Asn
 85 90 95

Asp Ile Glu Gly Arg Pro Leu Leu Thr Val Thr Ala Thr Gly Val Ile
 100 105 110

Gln Thr Arg Gln Tyr Glu Thr Ser Ser Leu Pro Gly Arg Leu Leu Ser

Arg Gly Glu Leu Gln His Val Thr Leu Val Lys Arg Asp Lys Gly Ala
 465 470 475 480
 Asn Asp Asp Arg Glu Trp Tyr Arg Tyr Ser Ser Asp Gly Arg Arg Ile
 485 490 495
 Leu Lys Ile Asn Glu Gln Gln Thr Ser Ser Asn Ser Gln Thr Gln Arg
 500 505 510
 Ile Thr Tyr Leu Pro Ser Leu Glu Leu Arg Leu Thr Gln Asn Ser Thr
 515 520 525
 Ile Thr Thr Glu Asp Leu Gln Val Ile Thr Val Gly Glu Ala Gly Arg
 530 535 540
 Ala Gln Val Arg Val Leu His Trp Asp Ser Gly Gln Pro Glu Asp Ile
 545 550 555 560
 Asp Asn Asn Gln Leu Arg Tyr Ser Tyr Asp Asn Leu Ile Gly Ser Ser
 565 570 575
 Gln Leu Glu Leu Asp Ser Lys Gly Glu Ile Ile Ser Glu Glu Glu Tyr
 580 585 590
 Tyr Pro Tyr Gly Gly Thr Ala Leu Trp Ala Thr Arg Lys Arg Thr Glu
 595 600 605
 Ala Ser Tyr Lys Thr Ile Arg Tyr Ser Gly Lys Glu Arg Asp Ala Thr
 610 615 620
 Gly Leu Tyr Tyr Tyr Gly Tyr Arg Tyr Tyr Gln Pro Trp Val Gly Arg
 625 630 635 640
 Trp Leu Ser Ala Asp Pro Ala Gly Thr Val Asp Gly Leu Asn Leu Tyr
 645 650 655
 Arg Met Val Arg Asn Asn Pro Val Thr Leu Leu Asp Pro Asp Gly Leu
 660 665 670
 Met Pro Thr Ile Ala Glu Arg Ile Ala Ala Leu Gln Lys Asn Lys Val
 675 680 685
 Ala Asp Ser Ala Pro Ser Pro Thr Asn Ala Thr Asn Val Ala Ile Asn
 690 695 700
 Ile Arg Pro Pro Val Ala Pro Lys Pro Thr Leu Pro Lys Ala Ser Thr
 705 710 715 720
 Ser Ser Gln Ser Thr Thr Tyr Pro Ile Lys Ser Ala Ser Ile Lys Pro
 725 730 735
 Thr Thr Ser Gly Ser Ser Ile Thr Ala Pro Leu Ser Pro Val Gly Asn
 740 745 750
 Lys Ser Thr Pro Glu Ile Ser Leu Pro Glu Ser Thr Gln Ser Asn Ser
 755 760 765
 Ser Ser Ala Ile Ser Thr Asn Leu Gln Lys Lys Ser Phe Thr Leu Tyr
 770 775 780
 Arg Ala Asp Asn Arg Ser Phe Glu Asp Met Gln Ser Lys Phe Pro Glu
 785 790 795 800
 Gly Phe Lys Ala Trp Thr Pro Leu Asp Thr Lys Met Ala Arg Gln Phe
 805 810 815

115 120 125
 Val Thr Glu Gln Ile Pro Glu Lys Thr Ser Arg Ile Thr Glu Arg Leu
 130 135 140
 Ile Trp Ala Gly Asn Ser Glu Ala Glu Lys Asn His Asn Leu Ala Ser
 145 150 155 160
 Gln Cys Val Arg His Tyr Asp Thr Ala Gly Val Thr Arg Leu Glu Ser
 165 170 175
 Leu Ser Leu Thr Gly Thr Val Leu Ser Gln Ser Ser Gln Leu Leu Ser
 180 185 190
 Asp Thr Gln Glu Ala Ser Trp Thr Gly Asp Asn Glu Thr Val Trp Gln
 195 200 205
 Asn Met Leu Ala Asp Asp Ile Tyr Thr Thr Leu Ser Ala Phe Asp Ala
 210 215 220
 Thr Gly Ala Leu Leu Thr Gln Thr Asp Ala Lys Gly Asn Ile Gln Arg
 225 230 235 240
 Leu Thr Tyr Asp Val Ala Gly Gln Leu Asn Gly Ser Trp Leu Thr Leu
 245 250 255
 Lys Asp Gln Pro Glu Gln Val Ile Ile Arg Ser Leu Thr Tyr Ser Ala
 260 265 270
 Ala Gly Gln Lys Leu Arg Glu Glu His Gly Asn Gly Val Ile Thr Glu
 275 280 285
 Tyr Ser Tyr Glu Pro Glu Thr Gln Gln Leu Ile Gly Thr Lys Thr His
 290 295 300
 Arg Pro Ser Asp Ala Lys Val Leu Gln Asp Leu Arg Tyr Glu Tyr Asp
 305 310 315 320
 Pro Val Gly Asn Val Ile Ser Ile Arg Asn Asp Ala Glu Ala Thr Arg
 325 330 335
 Phe Trp His Asn Gln Lys Val Ala Pro Glu Asn Thr Tyr Thr Tyr Asp
 340 345 350
 Ser Leu Tyr Gln Leu Ile Ser Ala Thr Gly Arg Glu Met Ala Asn Ile
 355 360 365
 Gly Gln Gln Ser Asn Gln Leu Pro Ser Leu Thr Leu Pro Ser Asp Asn
 370 375 380
 Asn Thr Tyr Thr Asn Tyr Thr Arg Thr Tyr Thr Tyr Asp Arg Gly Gly
 385 390 395 400
 Asn Leu Thr Lys Ile Gln His Ser Ser Pro Ala Thr Gln Asn Asn Tyr
 405 410 415
 Thr Thr Asn Ile Thr Val Ser Asn Arg Ser Asn Arg Ala Val Leu Ser
 420 425 430
 Thr Leu Thr Glu Asp Pro Ala Gln Val Asp Ala Leu Phe Asp Ala Gly
 435 440 445
 Gly His Gln Asn Thr Leu Ile Ser Gly Gln Asn Leu Asn Trp Asn Thr
 450 455 460

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Ala Ser Val Phe Ile Gly Gln Lys Asp Thr Ser Asn Leu Pro Lys Glu
 820 825 830
 Thr Val Lys Asn Ile Asn Thr Trp Gly Thr Lys Pro Lys Leu Asn Asp
 835 840 845
 Leu Ser Thr Tyr Ile Lys Tyr Thr Lys Asp Lys Ser Thr Val Trp Val
 850 855 860
 Ser Thr Ala Ile Asn Thr Glu Ala Gly Gly Gln Ser Ser Gly Ala Pro
 865 870 875 880
 Leu His Glu Ile Asn Met Asp Leu Tyr Glu Phe Thr Ile Asp Gly Gln
 885 890 895
 Lys Leu Asn Pro Leu Pro Arg Gly Arg Ser Lys Asp Arg Val Pro Ser
 900 905 910
 Leu Leu Leu Asp Thr Pro Glu Ile Glu Thr Ala Ser Ile Ile Ala Leu
 915 920 925
 Asn His Gly Pro Val Asn Asp Ala Glu Val Ser Phe Leu Thr Thr Ile
 930 935 940
 Pro Leu Lys Asn Val Lys Pro Tyr Lys Arg
 945 950

<210> 13
 <211> 2522
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 <213> Photorhabdus luminescens

<400> 13
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 Asp Val Leu Lys Ile Gln Cys Gly Phe Gln Cys Leu Thr Asp Ile Ser
 20 25 30
 His Ser Ser Phe Asn Glu Phe His Gln Gln Val Ser Glu His Leu Ser
 35 40 45
 Trp Ser Glu Ala His Asp Leu Tyr His Asp Ala Gln Gln Ala Gln Lys
 50 55 60
 Asp Asn Arg Leu Tyr Glu Ala Arg Ile Leu Lys Arg Thr Asn Pro Gln
 65 70 75 80
 Leu Gln Asn Ala Val His Leu Ala Ile Val Ala Pro Asn Ala Glu Leu
 85 90 95
 Ile Gly Tyr Asn Asn Gln Phe Ser Gly Arg Ala Ser Gln Tyr Val Ala
 100 105 110
 Pro Gly Thr Val Ser Ser Met Phe Ser Pro Ala Ala Tyr Leu Thr Glu
 115 120 125
 Leu Tyr Arg Glu Ala Arg Asn Leu His Ala Ser Asp Ser Val Tyr Arg
 130 135 140
 Leu Asp Thr Arg Arg Pro Asp Leu Lys Ser Met Ala Leu Ser Gln Gln
 145 150 155 160

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Asn Met Asp Thr Glu Leu Ser Thr Leu Ser Leu Ser Asn Glu Leu Leu
 165 170 175
 Leu Glu Ser Ile Lys Thr Glu Ser Lys Leu Asp Asn Tyr Thr Gln Val
 180 185 190
 Met Glu Met Leu Ser Ala Phe Arg Pro Ser Gly Ala Thr Pro Tyr His
 195 200 205
 Asp Ala Tyr Glu Asn Val Arg Lys Val Ile Gln Leu Gln Asp Pro Gly
 210 215 220
 Leu Glu Gln Leu Asn Ala Ser Pro Ala Ile Ala Gly Leu Met His Gln
 225 230 235 240
 Ala Ser Leu Leu Gly Ile Asn Ala Ser Ile Ser Pro Glu Leu Phe Asn
 245 250 255
 Ile Leu Thr Glu Glu Ile Thr Glu Gly Asn Ala Glu Glu Leu Tyr Lys
 260 265 270
 Lys Asn Phe Gly Asn Ile Glu Pro Ala Ser Leu Ala Met Pro Glu Tyr
 275 280 285
 Leu Arg Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser Gln Phe Ile
 290 295 300
 Gly Lys Ala Ser Asn Phe Gly Gln Gln Glu Tyr Ser Asn Asn Gln Leu
 305 310 315 320
 Ile Thr Pro Ile Val Asn Ser Asn Asp Gly Thr Val Lys Val Tyr Arg
 325 330 335
 Ile Thr Arg Glu Tyr Thr Thr Asn Ala Asn Gln Val Asp Val Glu Leu
 340 345 350
 Phe Pro Tyr Gly Gly Glu Asn Tyr Gln Leu Asn Tyr Lys Phe Lys Asp
 355 360 365
 Ser Arg Gln Asp Val Ser Tyr Leu Ser Ile Lys Leu Asn Asp Lys Arg
 370 375 380
 Glu Leu Ile Arg Ile Glu Gly Ala Pro Gln Val Asn Ile Glu Tyr Ser
 385 390 395 400
 Glu His Ile Thr Leu Ser Thr Thr Asp Ile Ser Gln Pro Phe Glu Ile
 405 410 415
 Gly Leu Thr Arg Val Tyr Pro Ser Ser Ser Trp Ala Tyr Ala Ala Ala
 420 425 430
 Lys Phe Thr Ile Glu Glu Tyr Asn Gln Tyr Ser Phe Leu Leu Lys Leu
 435 440 445
 Asn Lys Ala Ile Arg Leu Ser Arg Ala Thr Glu Leu Ser Pro Thr Ile
 450 455 460
 Leu Glu Ser Ile Val Arg Ser Val Asn Gln Gln Leu Asp Ile Asn Ala
 465 470 475 480
 Glu Val Leu Gly Lys Val Phe Leu Thr Lys Tyr Tyr Met Gln Arg Tyr
 485 490 495
 Ala Ile Asn Ala Glu Thr Ala Leu Ile Leu Cys Asn Ala Leu Ile Ser
 500 505 510

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Gln Arg Ser Tyr Asp Asn Gln Pro Ser Gln Phe Asp Arg Leu Phe Asn
 515 520 525
 Thr Pro Leu Leu Asn Gly Gln Tyr Phe Ser Thr Gly Asp Glu Glu Ile
 530 535 540
 Asp Leu Asn Pro Gly Ser Thr Gly Asp Trp Arg Lys Ser Val Leu Lys
 545 550 555 560
 Arg Ala Phe Asn Ile Asp Asp Ile Ser Leu Tyr Arg Leu Leu Lys Ile
 565 570 575
 Thr Asn His Asn Asn Gln Asp Gly Lys Ile Lys Asn Asn Leu Asn Asn
 580 585 590
 Leu Ser Asp Leu Tyr Ile Gly Lys Leu Leu Ala Glu Ile His Gln Leu
 595 600 605
 Thr Ile Asp Glu Leu Asp Leu Leu Leu Val Ala Val Gly Glu Gly Glu
 610 615 620
 Thr Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Ala Leu Ile Arg
 625 630 635 640
 Lys Leu Asn Thr Ile Thr Val Trp Leu Gln Thr Gln Lys Trp Ser Ala
 645 650 655
 Phe Gln Leu Phe Val Met Thr Ser Thr Ser Tyr Asn Lys Thr Leu Thr
 660 665 670
 Pro Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly Leu Gln Gly
 675 680 685
 Phe Asp Lys Asp Lys Ala Asn Leu Leu His Val Met Ala Pro Tyr Ile
 690 695 700
 Ala Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His Ser Val Leu
 705 710 715 720
 Leu Trp Ala Asp Lys Leu Lys Pro Gly Asp Gly Ala Met Thr Ala Glu
 725 730 735
 Lys Phe Trp Asp Trp Leu Asn Thr Gln Tyr Thr Pro Asp Ser Ser Glu
 740 745 750
 Val Leu Ala Thr Gln Glu His Ile Val Gln Tyr Cys Gln Ala Leu Ala
 755 760 765
 Gln Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu Asn Ala Phe
 770 775 780
 Arg Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ser Ser Thr Glu Ala
 785 790 795 800
 Val Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr Arg Phe Ala
 805 810 815
 Asp Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val Leu Ala Ala
 820 825 830
 Phe Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp Ala Met Asn
 835 840 845
 Leu Asp Ala Asn Leu Leu Leu Gln Ala Ser Thr Gln Ala Gln Asn His

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850	855	860
Gln His Leu Pro Pro Val Thr Gln Lys Asn Ala Phe Ser Cys Trp Thr 865 870 875 880		
Ser Ile Asp Thr Ile Leu Gln Trp Val Asn Val Ala Gln Gln Leu Asn 885 890 895		
Val Ala Pro Gln Gly Val Ser Ala Leu Val Gly Leu Asp Tyr Ile Gln 900 905 910		
Leu Asn Gln Lys Ile Pro Thr Tyr Ala Gln Trp Glu Ser Ala Gly Glu 915 920 925		
Ile Leu Thr Ala Gly Leu Asn Ser Gln Gln Ala Asp Ile Leu His Ala 930 935 940		
Phe Leu Asp Glu Ser Arg Ser Ala Ala Leu Ser Thr Tyr Tyr Ile Arg 945 950 955 960		
Gln Val Ala Lys Pro Ala Ala Ala Ile Lys Ser Arg Asp Asp Leu Tyr 965 970 975		
Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr 980 985 990		
Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val Asn Arg Thr 995 1000 1005		
Leu Glu Asn Val Glu Glu Asn Ala His Ser Gly Val Ile Ser Arg Gln 1010 1015 1020		
Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala 1025 1030 1035 1040		
Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile Asp Pro Thr 1045 1050 1055		
Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu Gln Ser Val 1060 1065 1070		
Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala Phe Met Ser 1075 1080 1085		
Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val Ile Ser Ala 1090 1095 1100		
Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr Phe Ile Gly 1105 1110 1115 1120		
Leu Ser Glu Thr Asp Thr Gly Glu Tyr Tyr Trp Arg Ser Val Asp His 1125 1130 1135		
Ser Lys Phe Ser Asp Gly Lys Phe Ala Ala Asn Ala Trp Ser Glu Trp 1140 1145 1150		
His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Arg Ser Thr Ile Arg Pro 1155 1160 1165		
Val Met Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu Gln Lys Glu 1170 1175 1180		
Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln Thr Glu Thr 1185 1190 1195 1200		

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Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr Asp Gly Thr
 1205 1210 1215
 Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Glu Lys Ile Ser Lys Leu
 1220 1225 1230
 Glu Leu Ala Lys Asn Lys Ala Pro Gly Leu Tyr Cys Ala Gly Tyr Gln
 1235 1240 1245
 Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln Asp Thr Leu
 1250 1255 1260
 Asp Ser Tyr Lys Thr Ala Ser Met Gln Gly Leu Tyr Ile Phe Ala Asp
 265 1270 1275 1280
 Met Glu Tyr Lys Asp Met Thr Asp Gly Gln Tyr Lys Ser Tyr Arg Asp
 1285 1290 1295
 Asn Ser Tyr Lys Gln Phe Asp Thr Asn Ser Val Arg Arg Val Asn Asn
 1300 1305 1310
 Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Asn Ser Arg Lys
 1315 1320 1325
 Gly Tyr Asp Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr Asn Gly Asp
 1330 1335 1340
 Ile Pro Thr Ile Ser Tyr Lys Ala Thr Ser Ser Asp Leu Lys Ile Tyr
 345 1350 1355 1360
 Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu Gly Gln Gln
 1365 1370 1375
 Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu Gly Asp Lys
 1380 1385 1390
 Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn Ser Ser Asn
 1395 1400 1405
 Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Asn Gly Asn Val Ser Gly
 1410 1415 1420
 Leu Ser Gln Gly Arg Leu Leu Phe His Arg Asp Thr Asn Tyr Ser Ser
 425 1430 1435 1440
 Lys Val Glu Ala Trp Ile Pro Gly Ala Gly Arg Ser Leu Thr Asn Pro
 1445 1450 1455
 Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu Asn Lys Pro
 1460 1465 1470
 Asn Asp Leu Lys Gln Tyr Val Tyr Met Thr Asp Ser Lys Gly Thr Ala
 1475 1480 1485
 Thr Asp Val Ser Gly Pro Val Asp Ile Asn Thr Ala Ile Ser Pro Ala
 1490 1495 1500
 Lys Val Gln Val Thr Val Lys Ala Gly Ser Lys Glu Gln Thr Phe Thr
 505 1510 1515 1520
 Ala Asp Lys Asn Val Ser Ile Gln Pro Ser Pro Ser Phe Asp Glu Met
 1525 1530 1535
 Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Ser Leu Asn Phe
 1540 1545 1550

Thr Asn Asn Ser Ala Ser Ile Asp Ile Thr Phe Thr Ala Phe Ala Glu
 1555 1560 1565
 Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro Ile Thr Arg
 1570 1575 1580
 Lys Val Ser Thr Asp Asn Ser Leu Thr Leu Arg His Asn Glu Asn Gly
 585 1590 1595 1600
 Ala Gln Tyr Met Gln Trp Gly Val Tyr Arg Ile Arg Leu Asn Thr Leu
 1605 1610 1615
 Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile Asp Thr Ile
 1620 1625 1630
 Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu Gly Lys Gly
 1635 1640 1645
 Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Pro Ser Thr His Gly
 1650 1655 1660
 Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val Asp Asn Asn
 665 1670 1675 1680
 Ser His Ile Ile Tyr Ser Gly Gln Leu Lys Asp Thr Asn Ile Ser Thr
 1685 1690 1695
 Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln Asp Tyr Ser
 1700 1705 1710
 Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp Gly Thr Trp
 1715 1720 1725
 Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val Thr Ile Asn
 1730 1735 1740
 Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val Leu Asn Asn
 745 1750 1755 1760
 Ile Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser Leu Tyr Phe
 1765 1770 1775
 Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln Arg Leu Leu
 1780 1785 1790
 His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys Tyr Val Trp
 1795 1800 1805
 Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn Tyr Gln Trp
 1810 1815 1820
 Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser Asp Pro Leu
 825 1830 1835 1840
 Asp Ser Val Asp Pro Asp Ala Val Ala Gln His Asp Pro Met His Tyr
 1845 1850 1855
 Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile Ala Arg Gly
 1860 1865 1870
 Asp His Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Asn Glu Ala Lys
 1875 1880 1885
 Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys Pro Tyr Leu

1890	1895	1900
Pro Leu Ser Thr Thr Trp Asn Asp Pro Arg Leu Asp Lys Ala Ala Asp 905	1910	1915 1920
Ile Thr Thr Gln Ser Ala His Ser Ser Ser Ile Val Ala Leu Arg Gln 1925	1930	1935
Ser Thr Pro Ala Leu Leu Ser Leu Arg Ser Ala Asn Thr Leu Thr Asp 1940	1945	1950
Leu Phe Leu Pro Gln Ile Asn Glu Val Met Met Asn Tyr Trp Gln Thr 1955	1960	1965
Leu Ala Gln Arg Val Tyr Asn Leu Arg His Asn Leu Ser Ile Asp Gly 1970	1975	1980
Gln Pro Leu Tyr Leu Pro Ile Tyr Ala Thr Pro Ala Asp Pro Lys Ala 985	1990	1995 2000
Leu Leu Ser Ala Ala Val Ala Thr Ser Gln Gly Gly Gly Lys Leu Pro 2005	2010	2015
Glu Ser Phe Met Ser Leu Trp Arg Phe Pro His Met Leu Glu Asn Ala 2020	2025	2030
Arg Ser Met Val Ser Gln Leu Thr Gln Phe Gly Ser Thr Leu Gln Asn 2035	2040	2045
Ile Ile Glu Arg Gln Asp Ala Glu Ala Leu Asn Ala Leu Leu Gln Asn 2050	2055	2060
Gln Ala Ala Glu Leu Ile Leu Thr Asn Leu Ser Ile Gln Asp Lys Thr 065	2070	2075 2080
Ile Glu Glu Leu Asp Ala Glu Lys Thr Val Leu Glu Lys Ser Lys Ala 2085	2090	2095
Gly Ala Gln Ser Arg Phe Asp Ser Tyr Ser Lys Leu His Asp Glu Asn 2100	2105	2110
Ile Asn Ala Gly Glu Asn Gln Ala Met Thr Leu Arg Ala Ser Ala Ala 2115	2120	2125
Gly Leu Thr Thr Ala Val Gln Ala Ser Arg Leu Ala Gly Ala Ala Ala 2130	2135	2140
Asp Leu Val Pro Asn Ile Phe Gly Phe Ala Gly Gly Gly Ser Arg Trp 145	2150	2155 2160
Gly Ala Ile Ala Glu Ala Thr Gly Tyr Val Met Glu Phe Ser Ala Asn 2165	2170	2175
Val Met Asn Thr Glu Ala Asp Lys Ile Ser Gln Ser Glu Thr Tyr Arg 2180	2185	2190
Arg Arg Arg Gln Glu Trp Glu Ile Gln Arg Asn Asn Ala Glu Ala Glu 2195	2200	2205
Leu Lys Gln Leu Asp Ala Gln Leu Lys Ser Leu Ala Val Arg Arg Glu 2210	2215	2220
Ala Ala Val Leu Gln Lys Thr Ser Leu Lys Thr Gln Gln Glu Gln Thr 225	2230	2235 2240

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Gln Ala Gln Leu Ala Phe Leu Gln Arg Lys Phe Ser Asn Gln Ala Leu
 2245 2250 2255
 Tyr Asn Trp Leu Arg Gly Arg Leu Ala Ala Ile Tyr Phe Gln Phe Tyr
 2260 2265 2270
 Asp Leu Ala Ile Ala Arg Cys Leu Met Ala Glu Gln Ala Tyr Arg Trp
 2275 2280 2285
 Glu Ile Ser Asp Asp Ser Ala Arg Phe Ile Lys Pro Gly Ala Trp Gln
 2290 2295 2300
 Gly Thr Tyr Ala Gly Leu Leu Ala Gly Glu Thr Leu Met Leu Ser Leu
 305 2310 2315 2320
 Ala Gln Met Glu Asp Ala His Leu Arg Arg Asp Lys Arg Ala Leu Glu
 2325 2330 2335
 Val Glu Arg Thr Val Ser Leu Ala Glu Ile Tyr Ala Gly Leu Pro Gln
 2340 2345 2350
 Asp Lys Gly Pro Phe Ser Leu Thr Gln Glu Ile Glu Lys Leu Val Asn
 2355 2360 2365
 Ala Gly Ser Gly Ser Ala Gly Ser Gly Asn Asn Asn Leu Ala Phe Gly
 2370 2375 2380
 Ala Gly Thr Asp Thr Lys Thr Ser Leu Gln Ala Ser Ile Ser Leu Ala
 385 2390 2395 2400
 Asp Leu Lys Ile Arg Glu Asp Tyr Pro Glu Ser Ile Gly Lys Ile Arg
 2405 2410 2415
 Arg Ile Lys Gln Ile Ser Val Thr Leu Pro Ala Leu Leu Gly Pro Tyr
 2420 2425 2430
 Gln Asp Val Gln Ala Ile Leu Ser Tyr Gly Asp Lys Ala Gly Leu Ala
 2435 2440 2445
 Asn Gly Cys Ala Ala Leu Ala Val Ser His Gly Thr Asn Asp Ser Gly
 2450 2455 2460
 Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys Phe Leu Pro Phe Glu Gly
 465 2470 2475 2480
 Ile Ala Ile Asp Gln Gly Thr Leu Thr Leu Ser Phe Pro Asn Ala Ser
 2485 2490 2495
 Thr Pro Ala Lys Gly Lys Gln Ala Thr Met Leu Lys Thr Leu Asn Asp
 2500 2505 2510
 Ile Ile Leu His Ile Arg Tyr Thr Ile Lys
 2515 2520

<210> 14

<211> 1481

<212> PRT

<213> Photorhabdus luminescens

<400> 14

Met Gln Asn Ser Gln Thr Phe Ser Met Thr Glu Leu Ser Leu Pro Lys
 1 5 10 15

Gly Gly Gly Ala Ile Thr Gly Met Gly Glu Ala Leu Thr Pro Ala Gly

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20	25	30
Pro Asp Gly Met Ala Ala Leu Ser Leu Pro Leu Pro Ile Ser Ala Gly		
35	40	45
Arg Gly Tyr Ala Pro Ser Leu Thr Leu Asn Tyr Asn Ser Gly Thr Gly		
50	55	60
Asn Ser Pro Phe Gly Leu Gly Trp Asp Cys Asn Val Met Thr Ile Arg		
65	70	75
Arg Arg Thr Ser Thr Gly Val Pro Asn Tyr Asp Glu Thr Asp Thr Phe		
	85	90
Leu Gly Pro Glu Gly Glu Val Leu Val Val Ala Leu Asn Glu Ala Gly		
100	105	110
Gln Ala Asp Ile Arg Ser Glu Ser Ser Leu Gln Gly Ile Asn Leu Gly		
115	120	125
Met Thr Phe Thr Val Thr Gly Tyr Arg Ser Arg Leu Glu Ser His Phe		
130	135	140
Ser Arg Leu Glu Tyr Trp Gln Pro Gln Thr Thr Gly Ala Thr Asp Phe		
145	150	155
Trp Leu Ile Tyr Ser Pro Asp Gly Gln Ala His Leu Leu Gly Lys Asn		
	165	170
Pro Gln Ala Arg Ile Ser Asn Pro Leu Asn Val Asn Gln Thr Ala Gln		
	180	185
Trp Leu Leu Glu Ala Ser Val Ser Ser His Gly Glu Gln Ile Tyr Tyr		
195	200	205
Gln Tyr Arg Ala Glu Asp Glu Thr Asp Cys Glu Thr Asp Glu Leu Thr		
210	215	220
Ala His Pro Asn Thr Thr Val Gln Arg Tyr Leu Gln Val Val His Tyr		
225	230	235
Gly Asn Leu Thr Ala Ser Glu Val Phe Pro Thr Leu Asn Gly Asp Asp		
	245	250
Pro Leu Lys Ser Gly Trp Leu Phe Cys Leu Val Phe Asp Tyr Gly Glu		
	260	265
Arg Lys Asn Ser Leu Ser Glu Met Pro Pro Phe Lys Ala Thr Ser Asn		
275	280	285
Trp Leu Cys Arg Lys Asp Arg Phe Ser Arg Tyr Glu Tyr Gly Phe Ala		
290	295	300
Leu Arg Thr Arg Arg Leu Cys Arg Gln Ile Leu Met Phe His Arg Leu		
305	310	315
Gln Thr Leu Ser Gly Gln Ala Lys Gly Asp Asp Glu Pro Ala Leu Val		
	325	330
Ser Arg Leu Ile Leu Asp Tyr Asp Glu Asn Ala Val Val Ser Thr Leu		
	340	345
Val Ser Val Arg Arg Val Gly His Glu Gln Asp Gly Thr Thr Ala Val		
355	360	365

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Ala Leu Pro Pro Leu Glu Leu Ala Tyr Gln Pro Phe Glu Pro Glu Gln
 370 375 380
 Lys Ala Leu Trp Arg Pro Met Asp Val Leu Ala Asn Phe Asn Thr Ile
 385 390 395 400
 Gln Arg Trp Gln Leu Leu Asp Leu Gln Gly Glu Gly Val Pro Gly Ile
 405 410 415
 Leu Tyr Gln Asp Lys Asn Gly Trp Trp Tyr Arg Ser Ala Gln Arg Gln
 420 425 430
 Thr Gly Glu Glu Met Asn Ala Val Thr Trp Gly Lys Met Gln Leu Leu
 435 440 445
 Pro Ile Thr Pro Ala Ile Gln Asp Asn Ala Ser Leu Met Asp Ile Asn
 450 455 460
 Gly Asp Gly Gln Leu Asp Trp Val Ile Thr Gly Pro Gly Leu Arg Gly
 465 470 475 480
 Tyr His Ser Gln His Pro Asp Gly Ser Trp Thr Arg Phe Thr Pro Leu
 485 490 495
 His Ala Leu Pro Ile Glu Tyr Thr His Pro Arg Ala Gln Leu Ala Asp
 500 505 510
 Leu Met Gly Ala Gly Leu Ser Asp Leu Val Leu Ile Gly Pro Lys Ser
 515 520 525
 Val Arg Leu Tyr Ala Asn Asn Arg Asp Gly Phe Thr Glu Gly Arg Asp
 530 535 540
 Val Val Gln Ser Gly Gly Ile Thr Leu Pro Leu Pro Gly Ala Asp Ala
 545 550 555 560
 Arg Lys Leu Val Ala Phe Ser Asp Val Leu Gly Ser Gly Gln Ala His
 565 570 575
 Leu Val Glu Val Ser Ala Thr Lys Val Thr Cys Trp Pro Asn Leu Gly
 580 585 590
 His Gly Arg Phe Gly Gln Pro Ile Thr Leu Pro Gly Phe Ser Gln Ser
 595 600 605
 Ala Ala Asn Phe Asn Pro Asp Arg Val His Leu Ala Asp Leu Asp Gly
 610 615 620
 Ser Gly Pro Ala Asp Leu Ile Tyr Val His Ala Asp His Leu Asp Ile
 625 630 635 640
 Phe Ser Asn Glu Ser Gly Asn Gly Phe Ala Gln Pro Phe Thr Leu Arg
 645 650 655
 Phe Pro Asp Gly Leu Arg Phe Asp Asp Thr Cys Gln Leu Gln Val Ala
 660 665 670
 Asp Val Gln Gly Leu Gly Val Val Ser Leu Ile Leu Ser Val Pro His
 675 680 685
 Met Ala Pro His His Trp Arg Cys Asp Leu Thr Asn Ala Lys Pro Trp
 690 695 700
 Leu Leu Ser Glu Met Asn Asn Met Gly Ala His His Thr Leu His
 705 710 715 720

Tyr Arg Ser Ser Val Gln Phe Trp Leu Asp Glu Lys Ala Ala Ala Leu
 725 730 735
 Ala Thr Gly Gln Thr Pro Val Cys Tyr Leu Pro Phe Pro Val His Thr
 740 745 750
 Leu Trp Gln Thr Glu Thr Glu Asp Glu Ile Ser Gly Asn Lys Leu Val
 755 760 765
 Thr Thr Leu Arg Tyr Ala His Gly Ala Trp Asp Gly Arg Glu Arg Glu
 770 775 780
 Phe Arg Gly Phe Gly Tyr Val Glu Gln Thr Asp Ser His Gln Leu Ala
 785 790 795 800
 Gln Gly Asn Ala Pro Glu Arg Thr Ser Pro Ala Leu Thr Lys Asn Trp
 805 810 815
 Tyr Ala Thr Gly Ile Pro Glu Val Asp Asn Thr Leu Ser Ala Gly Tyr
 820 825 830
 Trp Arg Gly Asp Thr Gln Ala Phe Thr Gly Phe Thr Pro His Phe Thr
 835 840 845
 Leu Trp Lys Glu Gly Lys Asp Val Pro Leu Thr Pro Glu Asp Asp His
 850 855 860
 Asn Leu Tyr Trp Leu Asn Arg Ala Leu Lys Gly Gln Pro Leu Arg Ser
 865 870 875 880
 Glu Leu Tyr Gly Leu Asp Gly Ser Ala Gln Gln Lys Ile Pro Tyr Thr
 885 890 895
 Val Thr Glu Ser Arg Pro Gln Val Arg Gln Leu Gln Asp Asn Thr Thr
 900 905 910
 Leu Ser Pro Val Leu Trp Ala Ser Val Val Glu Ser Arg Ser Tyr His
 915 920 925
 Tyr Glu Arg Ile Ile Ser Asp Pro Gln Cys Asn Gln Asp Ile Thr Leu
 930 935 940
 Ser Ser Asp Leu Phe Gly Gln Pro Leu Lys Gln Val Ser Val Gln Tyr
 945 950 955 960
 Pro Arg Arg Asn Lys Pro Thr Thr Asn Pro Tyr Pro Asp Thr Leu Pro
 965 970 975
 Asp Thr Leu Phe Ala Ser Ser Tyr Asp Asp Gln Gln Gln Leu Leu Arg
 980 985 990
 Leu Thr Tyr Gln Gln Ser Ser Trp His His Leu Ile Ala Asn Glu Leu
 995 1000 1005
 Arg Val Leu Gly Leu Pro Asp Gly Thr Arg Ser Asp Ala Phe Thr Tyr
 1010 1015 1020
 Asp Ala Lys His Val Pro Val Asp Gly Leu Asn Leu Glu Ala Leu Cys
 025 1030 1035 1040
 Ala Glu Asn Ser Leu Ile Ala Asp Asp Lys Pro Arg Glu Tyr Leu Asn
 1045 1050 1055
 Gln Gln Arg Thr Phe Tyr Thr Asp Gly Lys Thr Asp Gly Lys Asn Pro

1060	1065	1070
Thr Pro Leu Lys Thr Pro Thr Arg Gln Ala Leu Ile Ala Phe Thr Glu		
1075	1080	1085
Thr Ala Val Leu Thr Glu Ser Leu Leu Ser Ala Phe Asp Gly Gly Ile		
1090	1095	1100
Thr Pro Asp Glu Leu Pro Gly Leu Leu Thr Gln Ala Gly Tyr Gln Gln		
1105	1110	1115
Glu Pro Tyr Leu Phe Pro Leu Ser Gly Glu Asn Gln Val Trp Val Ala		
1125	1130	1135
Arg Lys Gly Tyr Thr Asp Tyr Gly Thr Glu Val Gln Phe Trp Arg Pro		
1140	1145	1150
Val Ala Gln Arg Asn Thr Gln Leu Thr Gly Lys Thr Thr Leu Lys Trp		
1155	1160	1165
Asp Thr His Tyr Cys Val Ile Thr Gln Thr Gln Asp Ala Ala Gly Leu		
1170	1175	1180
Thr Val Ser Ala Asn Tyr Asp Trp Arg Phe Leu Thr Pro Met Gln Leu		
1185	1190	1195
Thr Asp Ile Asn Asp Asn Val His Ile Ile Thr Leu Asp Ala Leu Gly		
1205	1210	1215
Arg Pro Val Thr Gln Arg Phe Trp Gly Ile Glu Asn Gly Val Ala Thr		
1220	1225	1230
Gly Tyr Ser Ser Pro Glu Ala Lys Pro Phe Thr Pro Pro Val Asp Val		
1235	1240	1245
Asn Ala Ala Ile Ala Leu Thr Gly Pro Leu Pro Val Ala Gln Cys Leu		
1250	1255	1260
Val Tyr Ala Pro Asp Ser Trp Met Pro Leu Phe Gly Gln Glu Thr Phe		
1265	1270	1275
Asn Thr Leu Thr Gln Glu Glu Gln Lys Thr Leu Arg Asp Leu Arg Ile		
1285	1290	1295
Ile Thr Glu Asp Trp Arg Ile Cys Ala Leu Ala Arg Arg Arg Trp Leu		
1300	1305	1310
Gln Ser Gln Lys Ala Gly Thr Pro Leu Val Lys Leu Leu Thr Asn Ser		
1315	1320	1325
Ile Gly Leu Pro Pro His Asn Leu Met Leu Ala Thr Asp Arg Tyr Asp		
1330	1335	1340
Arg Asp Ser Glu Gln Gln Ile Arg Gln Gln Val Ala Phe Ser Asp Gly		
1345	1350	1355
Phe Gly Arg Leu Leu Gln Ala Ala Val Arg His Glu Ala Gly Glu Ala		
1365	1370	1375
Trp Gln Arg Asn Gln Asp Gly Ser Leu Val Thr Lys Met Glu Asp Thr		
1380	1385	1390
Lys Thr Arg Trp Ala Ile Thr Gly Arg Thr Glu Tyr Asp Asn Lys Gly		
1395	1400	1405

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Gln Ala Ile Arg Thr Tyr Gln Pro Tyr Phe Leu Asn Asp Trp Arg Tyr
 1410 1415 1420

Val Ser Asp Asp Ser Ala Arg Lys Glu Ala Tyr Ala Asp Thr His Ile
 1425 1430 1435 1440

Tyr Asp Pro Ile Gly Arg Glu Ile Gln Val Ile Thr Ala Lys Gly Trp
 1445 1450 1455

Leu Arg Gln Asn Gln Tyr Phe Pro Trp Phe Thr Val Ser Glu Asp Glu
 1460 1465 1470

Asn Asp Leu Ser Ala Asp Ala Leu Val
 1475 1480

<210> 15
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide

<400> 15
 cgggatcoga tgattttaaa agg

23

<210> 16
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide

<400> 16
 gcgccattga tttgag

16

<210> 17
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide

<400> 17
 cattagaggt cgaacgtac

19

<210> 18
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide

<400> 18
 gagcgagctc ttacttaatg gtgtag

26

<210> 19

<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 19
cagcgcgctc catgcagaat tcacagac 28

<210> 20
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 20
ggcaatggca gcgataag 18

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 21
cattaacgca ggaagagc 18

<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 22
gacctcgagt tacacgagcg cgtcag 26